

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:00:13 ; Search time 1459.44 Seconds
(without alignments)
7917.015 Million cell updates/sec

Title: US-08-709-662-1

Perfect score: 747
Sequence: 1 CTGCAAGACAGCTACCATGA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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95: gb_rol2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	747	100.0	747	9 AR059956	AR059956 Sequence
2	747	100.0	766	94 MAU41738	U41738 Mesocricetu
3	599.8	80.3	747	9 AR054141	AR054141 Sequence
4	586	78.4	586	97 HSU41737	U41737 Human pancr
5	536	71.8	558	9 AR038161	AR038161 Sequence
6	459.8	61.6	762	94 AB035204	AB035204 Mus muscu
7	451.8	60.5	788	94 AB028625	AB028625 Mus muscu
8	296.6	39.7	760	93 HSHIP	X68641 H.sapiens H

9	296.6	39.7	784	97	HUMAPC	D13510	Homo sapiens
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11	296.6	39.7	797	97	SS1768	SS1768	PAP-H-Pancr
12	292.6	39.2	759	94	D63359	D63359	Mouse mRNA
13	287.2	38.4	798	9	AR076565	AR076565	Sequence
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21	279	37.3	793	10	113450	113450	Sequence 1
22	272.6	36.5	777	95	S77413	S77413	Rattus norv
23	269	36.0	773	94	D63357	D63357	Mouse mRNA
24	269	36.0	824	94	D63356	D63356	Mouse mRNA
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26	258.2	34.6	528	10	E07527	E07527	DNA sequenc
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28	255.6	34.2	522	9	AR076560	AR076560	Sequence
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42	145.4	19.5	598	89	AF172331	AF172331	Homo sapi
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ALIGNMENTS

RESULT	1
LOCUS	AR059956
DEFINITION	Sequence 1 from patent US 5840531.
ACCESSION	AR059956
VERSION	AR059956.1
KEYWORDS	GI:5986406
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 747) Vink,A.I., Pittenger,G.L., Rafaeloff,R., Rosenberg,L. and Duguid,W.P. <u>Ingap protein involved in pancreatic islet neogenesis</u> Patent: US 5840531-A 1 24-NOV-1998; Location/Qualifiers 1..747 Source
TITLE	JOURNAL
FEATURES	source
BASE COUNT	198 a 173 c 158 g 218 t
ORIGIN	/organism="unknown"

PAT 29-SEP-1998

bad date

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Best Local Similarity	100.0%;	Pred. No. 7.8e-200;		
Matches 747; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

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61 TTCCGCTGATGTTCCCTTTCTTGGGTGGAAGGTGMAAGATCTCAAAAGAACTGCTTC 120

Db	61	TTCCGCGCTGATGTTCCCTTTCTTGGGTGGAGAGTGAAGATCTCAAGAAAGAACTGCCCTTC	120
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Db	121	TTACAGTATTAACTGTCTCCTCAAGGCTGTGTAGCCTATGGGCTCTATTGGTATTCACTGAT	180
OY	181	TTTGGTATACCAGACAGACCTGGTCTAATGACGAAGTATCCGCGCAGATGCAATTTCTCAGSACA	240
Db	181	TTTGGTATACCAGACAGACCTGGTCTAATGACGAAGTATCCGCGCAGATGCAATTTCTCAGSACA	240
OY	241	CCTGCAATTTCTTCTTCAGTACTGCTGTAATTAACCTTTCGTGTCCTCCCTTGTGAAAGACAG	300
Db	241	CCTGCAATTTCTTCTTCAGTACTGCTGTAATTAACCTTTCGTGTCCTCCCTTGTGAAAGACAG	300
OY	301	TTTGAAGGCGCTAACAGTACATCTGATTTGGAGCTCATGATCCCTCACAATGTTACACTAC	360
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Db	481	TCAGAGTGGAGAGATTTTAAATTGTGAAAAATGAGCTTCCCTATATCTGCAAAATTCAGGT	540
OY	541	CTAGGGCAGTTCCTAATTTCCACAGCTTGAAAAATTTATGAAGCTCCACAATGGCAAGSAG	600
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OY	601	CAAGTATGAGATTTACTACACAGAAAGCAAGCTGTGCTACACACCACACCAATTTCCCT	660
Db	601	CAAGTATGAGATTTACTACACAGAAAGCAAGCTGTGCTACACACCACCAATTTCCCT	660
OY	661	TATATCATCTCTGCTGTTTTTCTATACGATATATCTGTGTGGCTGTAACTAAAGGCTC	720
Db	661	TATATCATCTCTGCTGTTTTTCTATACGATATATCTGTGTGGCTGTAACTAAAGGCTC	720
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Db	721	AGAGAACAATAAATATGTCATCTAAC	747

RESULT 2
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LOCUS MAU041738 766 bp mRNA
DEFINITION Mesocricetus auratus pancreatic beta cell growth factor (INGAP)
ACCESSION U041738
VERSION U041738
KEYWORDS U041738.1 GI:1514683
SOURCE golden hamster.
ORGANISM Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
REFERENCE 1 (bases 1 to 766)
AUTHORS Rafaelioff, R., Piltenger, G. L., Barlow, S. W., Qin, X. F., Yan, B.,
Rosenberg, L. and Vainik, A. I.
TITLE Cloning and sequencing of the pancreatic beta cell growth factor
gene (INGAP) and its expression in islet neogenesis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 766)
AUTHORS Vainik, A. I.
JOURNAL Direct Submission
TITLE Submitted (01-DEC-1995) Aaron I. Vainik, Eastern Virginia Medical
School, The Diabetes Institutes, 855 W. Brambleton Ave, Norfolk, VA
23510, USA

FEATURES
source

Location/Qualifiers
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/product="pancreatic beta cell growth factor"
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BASE COUNT 207 a 179 c 160 g 220 t
ORIGIN

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Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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740 AGAGACAAATAAATATGTCATCAAC 766
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RESULT 3
AR054141 747 bp DNA PAT 29-SEP-1999
LOCUS Sequence 1 from patent US 5834590.
DEFINITION AR054141
ACCESSION AR054141
VERSION AR054141.1 GI:5979003
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 747)
AUTHORS Vainik,A.I., Pittenger,G.L., Rafaeloff,R., Rosenberg,L. and
Duguid,W.P.
TITLE Ingap protein involved in pancreatic islet neogenesis
JOURNAL Patent: US 5834590-A 1 10-NOV-1998;
FEATURES Location/Qualifiers
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RESULT 4
LOCUS HSU41737 586 bp mRNA PRI 18-NOV-1997
DEFINITION Human pancreatic beta cell growth factor (INGAP) mRNA, complete cds.
ACCESSION U41737
VERSION U41737.1 GI:1514681
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 586)
AUTHORS Rafaeloff,R., Piltenger,G.L., Barlow,S.W., Qin,X.F., Yan,B., Rosenberg,L., Duguid,W.P. and Vink,A.I.
TITLE Cloning and sequencing of the pancreatic islet neogenesis associated protein (INGAP) gene and its expression in islet neogenesis in hamsters
JOURNAL J. Clin. Invest. 99 (9), 2100-2109 (1997)
MEDLINE 97296198
REFERENCE 2 (bases 1 to 586)
AUTHORS Vink,A.I.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1995) Aaron I. Vink, Eastern Virginia Medical School, The Diabetes Institutes, 855 W. Brambleton Ave, Norfolk, VA 23510, USA

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BASE COUNT 148 a 132 c 130 g 176 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.9e-154;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 84 GGGTGAAGGTGAAGATCTCAAAAGAACTGCTTCTACGATATACCTGTCTCAAG 143
Db 61 GGGTGAAGGTGAAGATCTCAAAAGAACTGCTTCTTACGATATACCTGTCTCAAG 120
Qy 144 GCTCTGAGCCTATGGGTCTCTATTGCTATTCACGATTTTGATACCAAGACCTGTGCTA 203

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Db 541 GCTTGAATAATTTATGAGAGCTCATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 586

RESULT 5
LOCUS AR038161 558 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5804421.
ACCESSION AR038161
VERSION AR038161.1 GI:5956878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 558)
AUTHORS Vink,A.I., Piltenger,G.L., Rafaeloff,Phall,R. and Barlow,S.W.
TITLE High level of expression of ingap in bacterial and eukaryotic cells
JOURNAL Patent: US 5804421-A 4 08-SEP-1998;
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source location/Qualifiers
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Best Local Similarity 99.1%; Pred. No. 2.4e-140;
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Qy 326 ATTGACTCATGATCCCTCATGATGTACACTACCAAGAGAGAGAGAGAGAGAGAGAG 385

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DEFINITION	Homo sapiens mRNA for PAP homologous protein, complete cds.	PRI	21-MAY-1999
ACCESSION	D13510		
VERSION	D13510.1 GI:285970		
KEYWORDS	PAP; pancreatitis-associated protein.		
SOURCE	Homo sapiens 20 years old cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Itoh T. and Terakura H.		
JOURNAL MEDLINE	Cloning and tissue-specific expression of cDNAs for the human and mouse homologues of rat pancreaticitis-associated protein (PAP) Biochim. Biophys. Acta 1172 (1-2), 184-186 (1993)		
COMMENT	Submitted (27-OCT-1992) to DDBJ by:		
	Takako Itoh		
	Shionogi Research Laboratories		
	Shionogi & Co., Ltd.		
	Fukushima-ku, Osaka 553		
	Japan		
	Phone: 06-458-5861 x376		
	Email: itoh@elab.shionogi.co.jp		
	Fax: 06-458-0987.		
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Dd	630 AGGACTCACCTGGAGAGAAATATTTCCTTAATTCCTCCCACTGACCACTCAT	684
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DEFINITION	Sequence 1 from patent US 5834214.	
ACCESSION	AR053327	
VERSION	AR053327.1	GI:5978189
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified. 1 (bases 1 to 797)	

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DEFINITION D63359
ACCESSION D63359.1 GI:1911090
KEYWORDS regIIbeta/PAP protein.
SOURCE Mus musculus (sub.species:domesticus, strain:C57BL/6J) adult male
pancreas cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Narushima,Y., Uno,M., Nakagawa,K., Mori,M., Miyashita,H.,
Suzuki,Y., Noguchi,N., Takasawa,S., Kumagai,T., Yonekura,H. and
Okamoto,H.
TITLE Structure, chromosomal localization and expression of mouse genes
encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma
JOURNAL Gene 185 (2), 159-168 (1997)
MEDLINE 97208868
REFERENCE 2 (bases 1 to 759)
AUTHORS Narushima,Y., Uno,M., Yonekura,H., Nakagawa,K., Mori,M.,
Miyashita,H., Suzuki,Y., Takasawa,S., Takeuchi,T. and Okamoto,H.
TITLE Structure, chromosomal localization, and expression of mouse
typeIII Reg genes, RegIIIalpha, RegIIbeta / PAP, RegIIgamma
JOURNAL Unpublished (1995)
REFERENCE 3 (bases 1 to 759)
AUTHORS Narushima,Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-1995) to the DDBJ/EMBL/GenBank databases. Yoichi
Narushima, Tohoku University School of Medicine, Biochemistry; 2-1
Setryo-machi, Aoba-ku, Sendai, Miyagi 980-77, Japan
(Tel.:022-717-8079, Fax:022-717-8083)
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DB 76 CTCCTGCTGATGCTCTTATCTCAGGTTCAAGGTGAAGTACCTCGAAGAAATATACCTTC 135
OY 121 TTCAGTATTAACCTGCTCCCTCAAGGCTGTAGCCATGAGGCTCATTTCTATTCACAT 180
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DB 316 AGGAACAGCTACCAATACATCTGATTTGGCTTCATGACCCCACTCGGGTGACAGAAC 375
OY 361 CAAGCAAGTGAAGTGAAGTGAAGCACTTCCATGCTGACCTTCTATTAACCTGGAGAG 420
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RESULT 13
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LOCUS AR076565
DEFINITION Sequence 12 from patent US 5959086.
ACCESSION AR076565
VERSION AR076565.1 GI:10003311
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 798)
AUTHORS Iovanna,J., Keln,V. and Dagorn,J.
TITLE Antibodies specific for human pancreatitis associated protein
JOURNAL Patent: US 5959086-A 12-28-SEP-1999;
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Db	155	TCCCGTCCCAAGAGGCTTCCAAAGGCTTATGAGCTCCACCTGCTATGACCCTTGTTTGTGCAC	21
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Db	455	CCACCATCTCAAGCCCCCGCCACCTGTGGAGCCTGTGGAGAGCAACGACTTCTGTAGGT	514
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DEFINITION	I13456	798 bp	DNA	PAT	26-JUL-1995
ACCESSION	I13456	Sequence 12 from patent US 5436169.			
VERSION	I13456.1	GI:910797			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 798)				
TITLE	Iovanna,J., Volker,K. and Dagorn,J.				
JOURNAL	Protein associated with acute pancreatitis agents for the screening				
FEATURES	of acute pancreatitis				
Source	Patent: US 5436169-A 12-25-JUL-1995;				
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BASE COUNT	181 a	213 c	198 g	206 t	
ORIGIN					

Query Match	38.4%	Score 287.2	DB 10	Length 798
Best Local Similarity	65.9%	Pred. No. 3.5e-70		
Matches 432, Conservative	0	Mismatches 223	Indels 1	Gaps 1

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OY 69 TGAGTCTTCCTTCTTGGGTGAAGGTGAAGAATCTCAAAGAACAATCGCTTCTTCACGTA 128
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DEFINITION	Human pancreaticitis associated protein mRNA, complete cds.
ACCESSION	M64337
VERSION	M64337.1 GI:189600
KEYWORDS	pancreatitis-associated protein; secretory pancreatic protein. Homo sapiens (library: lambda gII) pancreas cDNA to mRNA. Homo sapiens
SOURCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 798)
REFERENCE	O'Relle,B., Kelm,V., Meslotra,L., Dagorn,J. and Iovanna,J.L. Human pancreaticitis associated protein. Messenger RNA cloning and expression in pancreatic diseases
AUTHORS	J. Clin. Invest. (1992) in press
TITLE	Location/Qualifiers
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7/2

GenCore version 4.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Matches 308;	Conservative 0;	Mismatches 77;	Indels 0;	Gaps 0;
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107	GCTGATGTTCTCTTCTTGGGTGAGAGGTGAAGATCTCAAAAGAACTGCTTCTTAC	166		
126	GTTATACCTGTCCTCAAGGCTCTGTAGCCCTATGAGTCTTATGCTATTCACATGATTTGA	185		
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Db	CATTTCCTTCAGTACGTAGTGAATTTACCTTCGTCCTGCTTCTGCTTGAAGAACTTTGA	346		
287	CATTTCCTTCAGTACGTAGTGAATTTACCTTCGTCCTGCTTCTGCTTGAAGAACTTTGA	346		
306	CGGCTTACCAATACATCTGATGTGACTTCATGATTCCTCACAATGCTACACTACCAACG	365		
Db	CGGCTTACCAATACATCTGATGTGACTTCATGATTCCTCACAATGCTACACTACCAACG	406		
347	CCACATTCCTCCATACATCTGATGTGACTTCATGATTCCTCACAATGCTACACTACCAACG	406		
366	GAAGTGATGAGAGTGAGAGCTTC 390			
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407	AAATGATGAGAGTGAGAGCTTC 431			
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BF056837/c				
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DEFINITION	'7.1010d06.x1 NCI_CGAP_GG6 Homo sapiens cDNA clone IMAGE:3443771 3'			
ACCESSION	U00000.1			
VERSION	1.0			
KEYWORDS	NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
SOURCE	human.			
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 704)			
JOURNAL	NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgaps-remail.nih.gov			
	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael			
	R. Emmert-Buck, M.D., Ph.D.			
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima			
	Bonaldo, Ph.D.			
	cDNA Library Arrayed by: Greg Lennon, Ph.D.			
	DNA Sequencing by: Washington University Genome Sequencing Center			
	clone distribution: NCI-CGAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LML, send email to:			
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vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clones IDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
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Query Match      33.0%; Score 246.6; DB 143; Length 704;
Best Local Similarity 65.8%; Pred. No. 2.3e-63;
Matches 385; Conservative 0; Mismatches 198; Indels 2; Gaps 2;
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ORGANISM
Mus musculus
clone:2010205A03.
REFERENCE
AUTHORS
Carninci,P. and Hayashizaki,Y.
TITLE
High-efficiency full-length cDNA cloning
REFERENCE
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Katsunari,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,
Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,
Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsui,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.
TITLE
RIKEN integrated sequence analysis (RISA) system-384-Format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
REFERENCE
AUTHORS
The RIKEN genome Exploration Research Group Phase II Team and
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
REFERENCE
AUTHORS
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Carninci,P., Fukuda,S., Furukoshi,Y., Furuno,M.,
Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,D.,
Kojima,Y., Kono,H., Kouda,M., Koyama,S., Kuribara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Okazaki,Y.,
Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H.,
Sasaki,D., Shibata,K., Shibata,Y., Shindagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F.,
Tanaka,T., Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A.,
Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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ORGANISM	AK008608		
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AUTHORS	AK008608		
TITLE	AK008608		
JOURNAL	AK008608		
METHODS	AK008608		
DESCRIPTION	AK008608		
NOTES	AK008608		
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REFERENCE	2 (sites)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE REFERENCE	Genome Res. 10 (10), 1617-1630 (2000) 20499374
AUTHORS	3 (sites)
TITLE	Shibata,K., Itoh,M., Aizawa,K., Nagoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,T., Nishi,K., Kitunai,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.
JOURNAL MEDLINE REFERENCE	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913
AUTHORS	4 (sites)
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
JOURNAL MEDLINE REFERENCE	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 768)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Anno,H., Arai,A., Atakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Itawo,M., Kato,H., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Orido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gscl.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Best Local Similarity 66.6%: Pred. No. 1.5e-62;

Matches 365; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

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DB 73 CTCCTGCTGCTATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
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DB 433 GAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 489
OY 481 TCAGAGTGGAGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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DB 490 TCTGAAGTGGAGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 549
OY 541 CTAGGCA 548
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DB 550 CTAGGCA 557

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RESULT 7
AA871878 594 bp mRNA EST 16-MAR-1998
LOCUS vq42b08.r1 Bartschd howel MRLB9 Mus musculus cDNA clone
DEFINITION IMAGE:1096887.5, similar to gb:U15533.1 rat PANCREATITIS ASSOCIATED
PROTEIN 1 PRECURSOR (HUMAN); gb:D13509 Mouse mRNA for PAP
homologous protein (MOUSE);, mRNA sequence.
ACCESSION AA871878
VERSION AA871878.1 GI:2967323
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 594)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubaque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellingberg, K., Steptoe, M., Yan, F., Underwood, K., Moore, B.,
Theisling, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lml.gov) for further information.
MGI:603119
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 508.
Location/Qualifiers

FEATURES

source 1.594
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_1lib="IMAGE:1096887"
/clone_1lib="Bartschd howel MRLB9"
/tissue_type="bowel"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site 1: EcoRI; Site 2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTACGATCTGAGTGGAGCGGCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
[AATTGCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Source irradiated bowel harvested 72 hours after
irradiation (1400 Gys). Library constructed by Bob
Bartschd.

BASE COUNT 150 a 148 c 142 g 154 t
ORIGIN

Query Match 32.4%: Score 242; DB 13; Length 594;

Best Local Similarity 66.5%: Pred. No. 5.5e-62;

Matches 363; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

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OY 3 GCAGAGCAGTACATGATGCTTCCATGACCCCTCTGTAGATGCTTGTGATGCTGCT 62
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DB 14 GCAGAGCAGCAGATGCTTCCCGTATACCATCATCATGCTGCTGCTGCTGCT 73
OY 63 CCTGCTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 122
    |||||
DB 74 CCTGCTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 133
OY 123 CAGGTATACCTGCTCTCAAGGCTCTGTAGCCATGAGGCTCTATGCTTCTTCACTGATTT 182
    |||||
DB 134 CAGGTATACCTGCTCTCAAGGCTCTGTAGCCATGAGGCTCTATGCTTCTTCACTGATTT 193
OY 183 TGATACACAGACCTGCTTAAATGCAAGACTATCTGCTGCTGCTGCTGCTGCT 242
    |||||
DB 194 GTGTATCTAATAAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
OY 243 TGGCCTATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
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DB 254 TGTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
OY 303 TGAGGCTTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
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DB 314 GTTACAGTGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
OY 363 ACGAGATGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
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DB 374 ACGAGATGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
OY 423 ACCCTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
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DB 434 ATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 490
OY 483 AGAGTGGAGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
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DB 491 TGAAGTGGAGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
OY 543 ACGGCA 548

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Db 551 AGAGTA 556

RESULT 8
LOCUS A1621017/c 698 bp mRNA EST 14-DEC-1999
DEFINITION ts76a06.x1 NCI-CGAP GC6 Homo sapiens cDNA clone IMAGE:2237170 3'
similar to gb:U15533_rnal PANCREATITIS ASSOCIATED PROTEIN 1
PRECURSOR (HUMAN); mRNA sequence.
A1621017
ACCESSION A1621017.1 GI:4630143
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 698)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert length: 872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457
POLYA-No.

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2237170"
/clone_id="NCI-CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Plasmid DNA from the normalized library
NCI-CGAP_GC6 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clones 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 187 a 169 c 169 g 170 t 3 others

ORIGIN

Query Match 31.7%; Score 236.6; DB 22; Length 698;
Best Local Similarity 64.4%; Pred. No. 2.4e-60;
Matches 367; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

Db 691 GGTTCAGGGGAGAACCAAGAGGACGCTTCCTCCAGCTGTCACCAAG 632

QY 84 GGGTGGAGGTGAGAACTCTCAAAAGAACGCTCTTCTACAGCTATACCTGCTCAAG 143

Db 144 GCTGTAGCCTATGGGCTATTGCTATTCACGATTTGATACAGACAGCTGCTC- 202

QY 631 GCTCCAGGCTATGGCTCCCTCCCTGCTATGCTGTTTGTGACCAAAATTCGGAATG 572

Db 203 AATGCAAGATATCTGCTGCAAGATGCTTCAGACACCTGGCATTTCTCTCAGTACT 262

QY 571 GATGAGATCTGGCTTGCACAAAGGGCCCTCTGGAAAACTGTGTCTGTGCTCAGTGG 512

QY 263 GGTGAATTAACCTGCTGCTGCTCCTTGTGAGAAACAGTTTGACGGCTTACCAGTACATC 322

Db 511 GCTGAGGAGTCTGCTGCTGCTCCTGCTGAGAGACATTAAGACAGTACTCATACATC 452

QY 323 TGGATTGACATCCATGATCCCTCACATGATGACATACCAACGGAATGATGAAATG 382

Db 451 TGGATTGGGCTCCATGACCCGACACAGGAGCTCTGAGAGTGAAGATGAGGAGTGG 392

QY 383 AGCATTGCAATGCTGCTGACCTTATACAGTGGAGAGAAACCTCTATTTCTGCTGAC 442

Db 391 AGTACACTGATGATGATGATTAATCTTGCAATGGAGAAATCCTCCACATCTTAAC 332

QY 443 CGTGTATTTGTCAGATTGCTGTCAGAAATCAGGTTTTCAGAAAGTGGAGATTTTAAT 502

Db 331 CCTGGCCACTGGGAGGAGGCTGTGCAAGAACGACAGATTTTCAAGTGAAGATTAATAC 272

QY 503 TGTGAATAATGAGCTTCCCTATATATGCAAAATTCAGAGTCTAGGAGATTTTAATTCAC 562

Db 271 TGTGATGCAAGATTACCTATGTCTGCAAGTTCAAGGACTAGGCGAGTGGAGACTGAC 212

QY 563 AGCTGAATAATTTATGAAAGCTCACATGACAGAGAACATATGAGATTCACCTACAG 622

Db 211 AGCTTACCTTGGCGTGGACATCATGACATGACATGACACAGTGTGAAGACTACCTGG 152

QY 623 AAGACCAAGCTCTGCTACACACCCACAC 652

Db 151 AAGACAATATTTCTCCCAAACTGCCCTAC 122

RESULT 9
LOCUS AAI23026 626 bp mRNA EST 17-FEB-1997
DEFINITION mp82h07.r1 Soares thymus_2NBMT Mus musculus cDNA clone IMAGE:575773
5' similar to gb:U15533_rnal PANCREATITIS ASSOCIATED PROTEIN 1
PRECURSOR (HUMAN); gb:D13509 Mouse mRNA for PAP homologous protein
(MOUSE); mRNA sequence.
AAI23026
ACCESSION AAI23026.1 GI:1681077
VERSION EST.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM house mouse.
REFERENCE 1 (bases 1 to 626)
Marrta,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:350421
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 495.
Location/Qualifiers
1..626
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575773"
/clone_id="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"

AA140246	LOCUS	AA140246	526 bp	mRNA	EST	18-FEB-1997
DEFINITION		mq04f01.r1 Soares_thymus_2NBMT Mus musculus cDNA clone IMAGE:5777533				
REFERENCE		5' similar to gb:U1533_rnai PANCREATITIS ASSOCIATED PROTEIN 1				
AUTHORS		PRCUDSOR (HUMAN); gb:U13509 Mouse mRNA for PAP homologous protein (MUSE); mRNA sequence.				
ACCESSION		AA140246				
VERSION		AA140246.1	GI:1702682			
KEYWORDS		EST.				
SOURCE		house mouse.				
ORGANISM		Mus musculus				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
AUTHORS		1 (bases 1 to 526)				
		Marra,M., Hillier,D., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,				
		Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,				
		Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,				
		Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and				
		Waterston,R.				
TITLE		The WashU-HHMI Mouse EST Project				
JOURNAL		Unpublished (1996)				
COMMENT		Contact: Marra M/Mouse EST Project				
		WashU-HHMI Mouse EST Project				
		Washington University School of Medicine				
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
		Tel: 314 286 1800				
		Fax: 314 286 1810				
		Email: mouseest@watson.wustl.edu				
		This clone is available royalty-free through LNL; for further information.				
		IMAGE Consortium (info@image.llnl.gov)				
		MGI:352401				
		Seq primer: -28M13 rev2 from Amersham				
		High quality sequence stop: 491.				
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SOURCE		1..526				
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		/strain="C57BL/6J"				
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		/dev_stage="4 weeks"				
		/lab_host="DH10B"				
		/note="Vector: pT7T3-Pac (Pharmacia) with a modified				
		polylinker; Site_1: Not I - oligo(dT) primer [5',				
		TGTTACCAATCTGAAGTGGAGGCGGCCGCTTTTATTTTATTTTATTTT				
		3']; double-stranded cDNA was ligated to Eco RI adaptors				
		(Pharmacia), digested with Not I and cloned into the Not I				
		and Eco RI sites of the modified pT7T3 vector. RNA				
		provided by Dr. Bertrand Jordan. Library went through two				
		rounds of normalization, and was constructed by Bento				
		Soares and M.Fatima Bonaldo."				
BASE COUNT		130 a 130 c 129 g 137 t				
ORIGIN						
Query Match		28.5%; Score 213; DB 2; Length 526;				
Best Local Similarity		65.2%; P: Mismatches 180; Indels 5; Gaps 2;				
Matches 346; Conservative		0; Gaps 2;				
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1		GCAGACAGACAGATGCTTCCCTATTAACCATATACCATATGCTCCGAGATGCTGCTT				60
63		CTGCGCTGATGCTCTTCTTCTGGGTGGAAGGTGAAGAAATCTCAAAAGAACTGCTTCT				122
61		CTGCGCTGATGCTCTTCTTCTGAGTGAAGGTGAAGTGGCCAAAGAAAGATGCCCATCTT				120
123		CACGATATACCTGTCTCTCAAGGCTTGTAAGCTATAGGCTCTATGCTGATATACGATTT				182
121		CACGATGAGCGTCCCAAGGCTCCCGT--GCCTATGCTGCTATGCTATGCTGCTTTA				178

OY	183	TGATCCACAGACCGTGGCTATTCATGCAGAACAATTCTCGCAGATTCGATTTCTAGAGACC	242
Db	179	GGTATCTAAAAACTGGTATGATGCAGATATGGCTCGCCAAAAGGCCCTCAGACATC	238
OY	243	TGGCATTTCTTCTCAGTACTGGTGAAATAATTACCTTCGTGCTCCTCCCTTGGAAGAACGTT	302
Db	239	TTGTGTCTGTGTCTAGTGGCGCTGAAAGCTTCCTCTCTGCTCCATGTATCAAAACAGATG	298
OY	303	TGACGGCCTACCACTGACATCTGGATTGGACATCCATGATTCCTCCACATGATGACACTACCA	362
Db	299	GTAACAGTGGCCAAATATATGATGGATGGCTCCATGACCCGACACTGGGCGATATGAAACCA	358
OY	363	ACGGAAGTGGATGATGAAGGAGACACTTCCAAATGCTGCTCACTTCATATCAATGGAGAGA	422
Db	359	ACAGAGGTGGATGGAGATGGAGACATTCCTGATGTATGATTAATTCATCACTGAGGAGAGA	418
OY	423	ACCCTCTATTGCTGCTGACCCGCTGATTTATGTGACAGTTTTGTCTCGAAGATCAGGTTTC	482
Db	419	ATCCTTCTCTTCTCTCAG---GCAATCACTAGTGATGACCTGCAAGAGCCTCAGATTTTC	475
OY	483	AGAATGGAGAGATTTTATTTGTGAAATGACCTTCCTATATCTGCAAT	533
Db	476	TGAAGTGGAGAGCAATATTTGTTACTTAGACTTACCTGATGTCGCAAT	526
RESULT 15			
AKO08470			
LOCUS	AKO08470	659 bp mRNA	HNC 08-FEB-2001
DEFINITION	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010207102, full insert sequence.		
ACCESSION	AKO08470		
VERSION	AKO08470.1	GI:12842670	
KEYWORDS	CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone:lib.RIKEN full-length enriched mouse cDNA library clone:2010207102.		
ORGANISM	Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
REFERENCE			
AUTHORS	Carninci,P. and Hayashizaki,Y		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Methods Enzymol. 303, 19-44 (1999)		
REFERENCE			
AUTHORS			
TITLE	2 (sites)		
JOURNAL	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
REFERENCE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
AUTHORS	Genome Res. 10 (10), 1617-1630 (2000)		
TITLE	3 (sites)		
JOURNAL	Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Kituchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hatada,A., Yamamoto,R., Matsuno,H., Sekiguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Itawo,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.		
REFERENCE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer		
AUTHORS	Genome Res. 10 (11), 1757-1771 (2000)		
TITLE	4 (sites)		
JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.		
REFERENCE	Functional annotation of a full-length mouse cDNA collection		
AUTHORS	Nature 409, 685-690 (2001)		
TITLE	5 (bases 1 to 659)		
JOURNAL	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayashi,N., Hiramoto,C., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Itawa,M., Kato,H., Kawai,J.,		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:33:08 ; Search time 70.53 Seconds
(Without alignments)
2005.039 Million cell updates/sec

Title: US-08-709-662-1

Perfect score: 747
1 CTGCAAGACAGCTACCATCA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq:*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	2	US-08-709-662-1
2	599.8	80.3	747	2	US-08-401-530A-1
3	586	78.4	586	4	US-09-146-969-3
4	536	71.8	558	1	US-08-909-725-4
5	304.8	40.8	762	2	US-08-822-261-2
6	296.6	39.7	797	2	US-08-464-637-1
7	286.6	39.7	797	2	US-08-822-261-5
8	287.2	38.4	798	1	US-07-778-156-12
9	287.2	38.4	798	2	US-08-822-261-6
10	287.2	38.4	798	4	US-08-422-166-12
11	287.2	38.4	798	4	US-09-146-969-2
12	279	37.3	793	1	US-07-778-156-1
13	279	37.3	793	2	US-08-422-166-1
14	255.6	34.2	522	1	US-07-778-156-4
15	255.6	34.2	522	2	US-08-422-166-4
16	209.2	28.0	474	1	US-07-778-156-8
17	209.2	28.0	474	2	US-08-422-166-8
18	143.8	19.3	777	4	US-09-146-969-1
19	102.2	13.7	590	2	US-08-454-557C-32
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21	102.2	13.7	590	2	US-08-450-673C-32
22	102.2	13.7	590	5	PCT-US95-17111A-32
23	102	13.7	378	2	US-08-454-557C-16
24	102	13.7	378	2	US-08-340-426D-16
25	102	13.7	378	2	US-08-450-673C-16
26	102	13.7	378	5	PCT-US95-17111A-16
27	94	12.6	94	1	US-08-909-725-1

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29	73.4	9.8	306	2	US-08-422-166-9	Sequence 9, Appl
30	52.4	7.0	3411	4	US-09-146-969-4	Sequence 4, Appl
31	46.6	6.2	140	1	US-08-518-878B-8	Sequence 8, Appl
32	46.6	6.2	140	1	US-08-284-522B-8	Sequence 8, Appl
33	46.6	6.2	140	2	US-08-807-861A-8	Sequence 8, Appl
34	46.6	6.2	140	2	US-08-470-868A-8	Sequence 8, Appl
35	46.6	6.2	140	3	US-09-210-681-7	Sequence 8, Appl
36	46.6	6.2	140	3	US-08-946-719A-8	Sequence 8, Appl
37	45	6.0	140	1	US-08-518-878B-7	Sequence 8, Appl
38	45	6.0	140	1	US-08-284-522B-7	Sequence 7, Appl
39	45	6.0	140	2	US-08-807-861A-7	Sequence 7, Appl
40	45	6.0	140	2	US-08-470-868A-7	Sequence 7, Appl
41	45	6.0	140	3	US-09-210-681-7	Sequence 7, Appl
42	45	6.0	140	3	US-08-946-719A-7	Sequence 7, Appl
43	38.8	5.2	260	2	US-08-454-557C-88	Sequence 88, Appl
44	38.8	5.2	260	2	US-08-340-426D-88	Sequence 88, Appl
45	38.8	5.2	260	5	PCT-US95-17111A-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-709-662-1
Sequence 1, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vink, Aaron I.
APPLICANT: Piltenger, Gary E.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenber, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570, 59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541

US-08-709-662-1

Query Match 100.0%; Score 747; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 2,2e-236;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGCAAGACAGGATGACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
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DB 1 CTGCAAGACAGGATGACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
QY 61 TTCCGCTGATGCTGCTTCTTGGGTGGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
   |||||||
DB 61 TTCCGCTGATGCTGCTTCTTGGGTGGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
QY 121 TTACGATTAACCTGCTCTCAAGGCTGTAGCCTATGCTGCTATTCATTCATGAT 180
   |||||||
DB 121 TTACGATTAACCTGCTCTCAAGGCTGTAGCCTATGCTGCTATTCATTCATGAT 180
QY 181 TTGATATCCACAGACCTGCTATATGAGAACTATCCTGACAGATGCTTCTCAGGACA 240
   |||||||
DB 181 TTGATATCCACAGACCTGCTATATGAGAACTATCCTGACAGATGCTTCTCAGGACA 240
QY 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTCTGCTCCTTGTGAAGAACAG 300
   |||||||
DB 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTCTGCTCCTTGTGAAGAACAG 300
QY 301 TTGAGGCGCTACCACTGATCTGATGATGATGATGATGATGATGATGATGATGATG 360
   |||||||
DB 301 TTGAGGCGCTACCACTGATCTGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
   |||||||
DB 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
QY 421 GAACCCCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
   |||||||
DB 421 GAACCCCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 TCAGAGTGAAGATTTTAAATGTAATGATGATGATGATGATGATGATGATGATGATG 540
   |||||||
DB 481 TCAGAGTGAAGATTTTAAATGTAATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 CTGAGGAGTCTTAATTTCAACAGCTTGAATAATTTATGAAGCTCACATGAGCAAGAG 600
   |||||||
DB 541 CTGAGGAGTCTTAATTTCAACAGCTTGAATAATTTATGAAGCTCACATGAGCAAGAG 600
QY 601 CAAGTATGAGGATTCACCTGAGGAAGCAAGCTGCTGCTACACACCACCAATTCCT 660
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DB 601 CAAGTATGAGGATTCACCTGAGGAAGCAAGCTGCTGCTACACACCACCAATTCCT 660
QY 661 TATATATCTCTGCTGCTTCTTATCATCATGATATTCCTGCTGCTGATTAAGCTC 720
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DB 661 TATATATCTCTGCTGCTTCTTATCATCATGATATTCCTGCTGCTGATTAAGCTC 720
QY 721 AGAGAACAAATAATTAATGTCATCAAC 747
   |||||||
DB 721 AGAGAACAAATAATTAATGTCATCAAC 747
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RESULT 2

US-08-401-530A-1

; Sequence 1, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Piltenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC
; TITLE OF INVENTION: ISLET NEOGENESIS
; NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.48743

TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Cricetulus

FEATURE:

NAME/KEY: CDS
LOCATION: 20..541

US-08-401-530A-1

Query Match 80.3%; Score 599.8; DB 2; Length 747;
Best Local Similarity 87.7%; Pred. No. 6,7e-188;
Matches 655; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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QY 1 CTGCAAGACAGGATGACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
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DB 1 CTGCAAGACAGGATGACCTGATGCTTCCATGACCCCTGCTAGAGATGCTGATGCTGCT 60
QY 61 TTCCGCTGATGCTTCTTGGGTGGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
   |||||||
DB 61 TTCCGCTGATGCTTCTTGGGTGGAAGTGAAGAAATCTCAAAAGAACTGCTTC 120
QY 121 TTACGATTAACCTGCTCTCAAGGCTGTAGCCTATGCTGCTATTCATTCATGAT 180
   |||||||
DB 121 TTACGATTAACCTGCTCTCAAGGCTGTAGCCTATGCTGCTATTCATTCATGAT 180
QY 181 TTGATATCCACAGACCTGCTATATGAGAACTATCCTGACAGATGCTTCTCAGGACA 240
   |||||||
DB 181 TTGATATCCACAGACCTGCTATATGAGAACTATCCTGACAGATGCTTCTCAGGACA 240
QY 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTCTGCTCCTTGTGAAGAACAG 300
   |||||||
DB 241 CTTGGCATTTCTCTCAGTACTGCTGAATTAACCTTCTGCTCCTTGTGAAGAACAG 300
QY 301 TTGAGGCGCTACCACTGATCTGATGATGATGATGATGATGATGATGATGATGATG 360
   |||||||
DB 301 TTGAGGCGCTACCACTGATCTGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
   |||||||
DB 361 CAACGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
QY 421 GAACCCCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
   |||||||
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|||||
Db 421 GAACCCCTATTCCTGCTGACCGTGGTATTTGTCAGATTGTCGAGAAATCAGGTTT 480
OY 481 TCAGAGGAGGAGATTTTATTTGTAAGAAATGACCTCCCTATATTCGCAATTCAGGT 540
Db 481 TCAGAGGAGGAGATTTTATTTGTAAGAAATGACCTCCCTATATTCGCAATTCAGGT 540
OY 541 CTAGAGGAGTTCATTTTCAACAGCTTGAAATATTTATGAGCTCATGTGACAGAGAG 600
Db 541 CTAGAGGAGTTCATTTTCAACAGCTTGAAATATTTATGAGCTCATGTGACAGAGAG 600
OY 601 CAAGTATGAGGATTCACCTCAGAGAGAGCAGCTGCTCCTACACACCACCAATTCCT 660
Db 601 TTAATCATCT 660
OY 661 TATATCATCT 720
Db 661 AAGTATGAGGATTCACCTCAGAGAGAGCAGCTGCTCCTACACACCACCAATTCCT 720
OY 721 AGAGACAAAAATATAATGTCATCAAC 747
Db 721 AGAGACAAAAATATAATGTCATCAAC 747

RESULT 3
US-09-146-969-3
; Sequence 3, Application US/09146969
; Patent No. 6228585
; GENERAL INFORMATION:
; APPLICANT: Dieckgrafe, Brian K.
; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
; FILE REFERENCE: 04255.75314
; CURRENT APPLICATION NUMBER: US/09/146, 969
; CURRENT FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-969-3

Query Match 78.4%; Score 586; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 2, 1e-183;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TTCCATGACCCCTCTGATGATGCTTGGAGCTGCTTCTGCTGCTGATGCTTCTTCT 83
Db 1 ttccatgacctctctgagatgcttggagctgcttctgctgctgctgctgcttcttct 60
OY 84 GGGTGAAGGAGGAATCTCAAAAGAACTGCTTCTTCACTGATTAACCTGCTCTCAAG 143
Db 61 ggggtgaaggaggaatctcaaaagaactgcttcttcaactgataaactgcttctcaag 120
OY 144 GCTGTAGGCTATGAGGCTGATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 203
Db 121 gctctgagcctatgagcctgagcctatgagcctatgagcctatgagcctatgagc 180
OY 204 ATGAGAGACTATCTGCGAGATGATTTCTCAGAGACCTGCAATTTCTTCTCAGTACT 263
Db 181 atgagagactatctgagcctatgagcctatgagcctatgagcctatgagcctatgag 240
OY 264 GTGAATATTCCTGCTGCTCTCTCTGTAAGAACTGAGCGCTTACAGTACATCT 323
Db 241 gtgaatatctctgctgctctctctgtaagaactgagcgcttaccagatacatct 300
OY 324 GGATTTGACTGATGATGCTTCAATGCTATGCTATGCTATGCTATGCTATGCTATGCT 383
Db 301 ggatttgactgactgactgactgactgactgactgactgactgactgactgactgact 360
OY 384 GCACCTCAATGTGCTGATCTTCTATTAAGTGAGAGAGAACCTCTATTTCTCTGACC 443
Db 384 gcacctcaatgtgctgacttctatataagtgagagagaaacctctatttctctgacc 443

Db 361 gcaatccaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 420
OY 444 GTGGTATTTGAGATTTTGTCTCAGAAATCAGGTTTTCAGAGTGAGAGATTTTATTT 503
Db 421 gtggtatgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 480
OY 504 GTGAATGAGCTTCTCTATATTCGCAATTCAGGTTCTAGGAGTTCATATTTCAACA 563
Db 481 gtgaatgagcttctctatattctgcaaatcgaatcgaatcgaatcgaatcgaatcga 540
OY 564 GCTTGAATATTTATGAGCTTCATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609
Db 541 gcttgaatatattatgagcttcacatgagcagagagagagagagagagagagagag 586

RESULT 4
US-08-909-725-4
; Sequence 4, Application US/08909725
; Patent No. 5804421
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Pittenger, Gary
; APPLICANT: Rafeloff-Phall, Ronit
; APPLICANT: Barlow, Scott
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
; TITLE OF INVENTION: INGP IN BACTERIAL AND EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,725
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,096
; FILING DATE: 30-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32,145
; REFERENCE/DOCKET NUMBER: 0570,05173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELETYPE: 97430 BMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 558 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-909-725-4

Query Match 71.8%; Score 536; DB 1; Length 558;
Best Local Similarity 99.1%; Pred. No. 5, 9e-167;
Matches 539; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 86 GTGAGAGGTGAAGATCTCAAAAGAACTGCTTCTTACGATATTAACCTGCTCTCAAGC 145
Db 3 GCGGATCCCGAAGATCTCAAAAGAACTGCTTCTTACGATATTAACCTGCTCTCAAGC 62
OY 146 TCTGTAGCTATGAGGCTCTATTTGATTAACCTGATGATTTGATTAACCAAGAGACTGCTAT 205
Db 146 tctgtagctatgaggtctctatttgatttaacctgattgattttgatttaaccagagactgctat 205

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|||||
Db 63 TCTTACCTATGGGCTCTATTCATTCACATGATTTGTGATACACAGACCTGCTAAT 122
QY 206 GCNAATATCTCCCGCATGATCTTCAGAGACCTGGATTTCTTCAGTACGT 265
Db 123 GCAGATATCTCCCGCATGATCTTCAGAGACCTGGATTTCTTCAGTACGT 182
QY 266 GAAATTCATCTGCTCCCTCTGTGAAGACAGTTTGAAGGCTTACATCTGG 325
Db 183 GAAATTCATCTGCTCCCTCTGTGAAGACAGTTTGAAGGCTTACATCTGG 242
QY 326 ATTGAGATCATGATCCCTCATGATGTACACTACCAACGAAATGGAAGTGGAGC 385
Db 243 ATTGAGATCATGATCCCTCATGATGTACACTACCAACGAAATGGAAGTGGAGC 302
QY 386 AGTTCCATATGCTGACCTCTTATTAATGAGAGAACCCCTTATTTGCTGACCGT 445
Db 303 AGTTCCATATGCTGACCTCTTATTAATGAGAGAACCCCTTATTTGCTGACCGT 362
QY 446 GGTATTTGTCAGTTTGTCTCAGAAATCAGTTTTCAGAAAGTGGAGATTTAATTTGT 505
Db 363 GGTATTTGTCAGTTTGTCTCAGAAATCAGTTTTCAGAAAGTGGAGATTTAATTTGT 422
QY 506 GAAATGAGCTCCCTATATCTGCAATTCAGGCTTAGGGCAGTTCTAATTTTCACAGC 565
Db 423 GAAATGAGCTCCCTATATCTGCAATTCAGGCTTAGGGCAGTTCTAATTTTCACAGC 482
QY 566 TTGAAATATTTATGACCTCATGATGAGCAAGAGCAAGATGTAGGATTCACTCAGAG 625
Db 483 TTGAAATATTTATGACCTCATGATGAGCAAGAGCAAGATGTAGGATTCACTCAGAG 542
QY 626 AGCA 629
Db 543 AGCA 546

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RESULT 5
US-08-822-261-2
; Sequence 2, Application US/08822261
; Patent No. 5935813
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,261
; FILING DATE: Filed Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0251 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ISLNOT01
; CLONE: 2072483
US-08-822-261-2

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Query Match 40.8%; Score 304.8; DB 2; Length 762;
Best Local Similarity 67.1%; Pred. No. 9, 8e-91;
Matches 432; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

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QY 9 CAGTACCATGATGCTTCCTCATACCCCTCTGTAGATGTTTGGATGCTTCTGCG 68
Db 106 CAGACACTATGCTGCTCCCATGCGCTGCCAGTGTGCTGGATGCTGCTTCTGCG 165
QY 69 TGATGTTCCCTTCTGCGGTGAGTGAAGATCTCAAAAGAAAGTCCCTTCTTCAGTA 128
Db 166 TCAATTCCTCTGTCTCAGGTTCAGGTGAAGAAACCCAGAGACTGCTTCTCCAGCA 225
QY 129 TAACTGTCTCAGAGCTCTGTAGCTATGCTCTATTCATTCATGATTTTGATAC 188
Db 226 TCAGCTGTCCCAAGAGCTCCAGGCTATGCTCCCTCTATGCTTGTGTCAC 285
QY 189 CACAGACCTGCTTAATGCAAACTATCTGCCAGATGATTTTCTAGACACCTGGCAT 248
Db 286 CAAATTCCTGGATGATGCAATCTGCTGCGCAAGAGCGCCCTTGCAAACTGCTGT 345
QY 249 TTCTCTCAGTACTGCGAATTAATTCCTGCTGCTCCTCCTTGTGAAGAACAGTTTGACG 308
Db 346 CTGTGCTCAGTGGGCTGAGGAGATCCTGTGTCTCTCCTGCTGAGAGACTTATGTAACA 405
QY 309 CCTACAGTACATCTGATTTGACCTCATGATCCCTCAGATGCTACATCCCAAGGAA 368
Db 406 GCTACTCATCATCTGATGATTTGGGCTCATGACCCACACAGGCTCTGAGCCTGATGAG 465
QY 369 GTGATGGAAGTGGAGCAGTCCCATGCTGCTGACCTTCTATCTAGCTGGAGAGAACCCCT 428
Db 466 ATGATGGAAGTGGAGCAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 525
QY 429 CTATTCCTGCTGACCTGCTGATTTGTCAGATTTTGTCTCAGAAATGAGTTTTCAGAA 488
Db 526 CCACCATCTTAAACCTGGCCTGCTGAGGCTGTCAAGAACACAGATTTCTGAAGT 585
QY 489 GGAGAGATTTTAATGTAATGAAATGAGCTTCCCTATATCTGCAAAATTCAGAGTCTAGGCA 548
Db 586 GGAAGATTTTAATGTAATGAAATGAGCTTCCCTATATCTGCAAAATTCAGAGTCTAGGCA 645
QY 549 GTTCTATTTCAACACCTTGAATAATATATGAGCTCAGATGACAGCAAGCAAGCAATAG 608
Db 646 GTTGGAGATGACAGCCTTCAGCTTGGCGGCTGATCATGATGATGATGATGATGATGAT 705
QY 609 AGGATTCATCTCAGAGAGCAAGCTGCTGCTACACACCAAGCACC 652
Db 706 AAGACTCACCCTGGAAGAGAAATTTCTCCCAACACTGCGCTTACC 749

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RESULT 6
US-08-464-637-1
; Sequence 1, Application US/08464637
; Patent No. 5834214
; GENERAL INFORMATION:
; APPLICANT: Iovanna, Juan-Lucio
; APPLICANT: Dagorn, Jean-Charles
; APPLICANT: Keim, Volker
; APPLICANT: Sarles, Jacques
; TITLE OF INVENTION: Detection of Pancreatitis-Associated
; TITLE OF INVENTION: Protein for Diagnosis of Cystic Fibrosis or Pancreatic
; NUMBER OF SEQUENCES: 2

```


ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: pancreas
FEATURES:
NAME/KEY: CDS
LOCATION: 62..613
US-07-778-156-1

Query Match 37.3%, Score 279; DB 1; Length 793;
Best Local Similarity 65.6%; Pred. No. 3.2e-82;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

OY 5 AAGACAGTACCATGATGCTTCCATGACCCCTGATGATGCTGATGCTGCTTCC 64
DB 50 ATGAGAGTTAATATGTTGATGCTTGGCTCCAGTATGCTGATGCTGCTGCTCC 109
OY 65 TGCCGATGCTCTTCTTGGGTGAGAGTGAAGATCTCAAAAGAACTGCTTCA 124
DB 110 TGCCGATGCTCTTCTTACAGAGTGAAGAGACTCTCCGAAATAATACCTCTCA 169
OY 125 GGTATACCTGCTCTCAAGCTCTGATGCTTGGCTCTATGCTATGCTGATTTG 184
DB 170 CGCATGATGCTCCCAAGAGCTCCAGCATATGCTCTGATGCTGCTGCTGCTG 229
OY 185 ATACACAGACCTGCTTAATGCAACTATCCCTCCAGATGCTTCTCAGAGACCTG 244
DB 230 ATACACAGACCTGCTTGAATGCAACTGCTCCAGAAAGACCTGAAAGACCTT 289
OY 245 GCAATTTCTCAGACTGCTGAATTAATGCTGCTGCTGCTGCTGCTGCTGCTG 304
DB 290 GATGCTGCTCAATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 349
OY 305 ACGGCTACCATGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 350 AACACCTACCATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 409
OY 365 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
DB 410 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 469
OY 425 CCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484
DB 470 CCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
OY 485 AAGTGAGAGATTTTAAATGTAAGATG-AGCTTCCATATATCTGCAAAATCAAGTCTA 543
DB 530 AGATGAGAGATATACCAATGTAAGTGAAGTGGCTGACGCTGCAAAATTAAGTGA 589
OY 544 GGGAGGTTCTAATTTCAACAGCTTGAAATATATTAAGAGCTGACATGCAAGAGCA 603
DB 590 AAATTAACAGACAGCAACAGCTTGAATTTGCTGCAAGAGCAATCTGTCAGAGGGGCA 649
OY 604 GTATGAGATTCATCTGAGAGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 646
DB 650 ATATGAAGACTTGGCTAGAAAGATGTTATTTCTATCTACAGTCC 692

RESULT 13
US-08-422-166-1
Sequence 1, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:

APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
TITLE OF INVENTION: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:

ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: rat
TISSUE TYPE: pancreas

FEATURES:

NAME/KEY: CDS
LOCATION: 62..613
US-08-422-166-1

Query Match 37.3%, Score 279; DB 2; Length 793;
Best Local Similarity 65.6%; Pred. No. 3.2e-82;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

OY 5 AAGACAGTACCATGATGCTTCCATGACCCCTGATGATGCTGATGCTGCTTCC 64
DB 50 ATGAGAGTTAATATGTTGATGCTTGGCTCCAGTATGCTGATGCTGCTGCTCC 109
OY 65 TGCCGATGCTCTTCTTGGGTGAGAGTGAAGATCTCAAAAGAACTGCTTCA 124
DB 110 TGCCGATGCTCTTCTTACAGAGTGAAGAGACTCTCCGAAATAATACCTCTCA 169
OY 125 GGTATACCTGCTCTCAAGCTCTGATGCTTGGCTCTATGCTATGCTGATTTG 184
DB 170 CGCATGATGCTCCCAAGAGCTCCAGCATATGCTCTGATGCTGCTGCTGCTG 229
OY 185 ATACACAGACCTGCTTAATGCAACTATCCCTCCAGATGCTATGCTGCTGCTG 244


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1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: Patent In Release #1.0, Version #1.25
3
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/422,166
6 FILING DATE: 14-APR-1995
7 CLASSIFICATION: 435
8
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/778,156
11 FILING DATE: 19-DEC-1991
12
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Oblon, No. 5959086man F.
15 REGISTRATION NUMBER: 24,618
16 REFERENCE/DOCKET NUMBER: 354-012-0 PCT
17
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (703)521-4500
20 TELEFAX: (703)486-2347
21 TELEX: 248885 OPAT UR
22
23 INFORMATION FOR SEQ ID NO: 4:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 522 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: unknown
29 TOPOLOGY: unknown
30
31 MOLECULE TYPE: CDNA
32 ORIGINAL SOURCE:
33 ORGANISM: Homo sapiens
34 TISSUE TYPE: pancreas
35
36 US-08-422-166-4

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Job time: 3114 sec

Query Match	34.2%	Score 255.6;	DB 2,	Length 522;
Best Local Similarity	68.3%	Pred. No. 1.3e-74;		
Matches 354; Conservative	0;	Mismatches 164;	Indels 0;	Gaps 0

QY	17	ATGATGCTTCCCATGACCCTCTGTAGAGATCTGGATGCGCTTCCTCCGATGTC	76
Db	1	ATGCTGCTCCCATGAGCCCTCTGCCAGTGATCTTTTGATGCTCTTCCTCATGCTG	60
QY	77	CTTTCTTGGGTGGAAGGTGGAAGATCTCAAAAGAAATCGCTCTTCCACGATATACCTGT	136
Db	61	CTGTCTCAGGTTCAAGGTGGAAGAACCCAGAGGGAACCTGCGCTCTGCACGGAATCCGCTG	120
QY	137	CCTCAAGGCTCTGTAGCCATGAGGCTCTATTGCTATTCACTGATTTTGGATACCAAGACC	196
Db	121	CCCAAGGCTCTCAAGGCTCTATGAGCTCCACGCTATGCTTTGTTTGTGCACCAAAATCC	180
QY	197	TGGTCTATGGAAGACATCTCGTCAATGCAATTTCTCAGAGACCTCGGATTTCTCTC	256
Db	181	TGGACAGATGCAAGTCTGGCGCTGCCAAGAACGGCCCTCTGTAAACCTCGTCTGTGCTC	240
QY	257	AGTACTGGTGAATTAACCTTGTCCTCCCTGTGTGAAGAAAGTTGACAGGCGCTACACG	316
Db	241	AGTGGGCTGTAGGGATCTCTTGTCCTCTCCCTGTGTAAGAGCAATGGTAACAGCTACTCA	300
QY	317	TACATCTGGATTGGAGTCCATGATCCCTCAACATGTAACATACCACAGGAAGTGATGG	376
Db	301	TACGCTCTGATTTGGGCTTCATGACCCACACAGAGGCAACGCCCAATGGAAGAGGTTGG	360
QY	377	AAGTGAAGCACTTCCATGTCGTACCTTCTATTAACHTGGAGAGGAAGCCCTCTATTGGCT	436
Db	361	GAGTGAAGTACCACTGATGATGATGAATTACTTGTGCATGGGAGAGAAATCCCTCACATTC	420
QY	437	GCTGACCGTGTATTGTGCAAGTTTGTCTCAGAAATCAGGTTTTCAAGAGTGAGAGAT	496
Db	421	TCAAGCCCCGGCCACTGTGGCAGGCTCTCGAAGAGCACACACTTTTTCAGAGTGGAAGAT	480
QY	497	TTTAATTGTGAAGATGAGCTTCCCTATATCGCAAAAT	534
Db	481	TATACTGTAATGTAGAGTTACCTTAATGTGCAAAAT	518

Search completed: August 14, 2001, 16:25:02

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 15:35:18 ; Search time 104.73 Seconds
(without alignments)
4478.588 Million cell updates/sec

Title: US-08-709-662-1
Perfect score: 747
Sequence: 1 CTGCAAGACAGCTACCATGA.....AAAATAAATGTCATCAAC 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues
Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601.*
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22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	17	AA136612
2	586	78.4	586	21	AA299822
3	536	71.8	536	19	AAV46422
4	536	71.8	536	19	AAV30284
5	304.8	40.8	763	19	AAV58279
6	304.8	40.8	859	20	AAZ34271
7	304.8	40.8	859	21	AACT8569
8	286.6	39.7	797	15	AAO69201
9	296.6	39.7	940	21	AACT7777
10	291	39.0	756	19	AAV5234
11	287.2	38.4	798	12	AAQ14623

Result No.	Score	Query Match	Length	ID	Description
12	287.2	38.4	798	21	AA299821
13	286.8	38.4	781	20	AAZ26126
14	286.8	38.4	781	21	AAZ5486
15	279	37.3	793	12	AAQ14621
16	260.8	34.9	528	15	AAO64172
17	258.2	34.6	528	15	AAO64171
18	255.6	34.2	522	12	AAQ14619
19	245.4	32.9	790	11	AAO05300
20	212.4	28.4	602	21	AAI16252
21	209.2	28.0	474	12	AAQ14620
22	182.4	24.4	461	21	AACT8317
23	153.8	20.6	836	20	AAZ41387
24	153.8	20.6	845	21	AAZ41387
25	145.4	19.5	800	22	AAZ75077
26	145.4	19.5	843	21	AACT7946
27	145.4	19.5	843	22	AAZ75090
28	143.8	19.3	777	21	AAZ99820
29	141	18.9	749	9	AAAB1961
30	137.8	18.4	495	10	AAAB1109
31	137.8	18.4	498	9	AAAB1962
32	135	18.1	495	9	AAAB1181
33	134.6	18.0	495	10	AAAB1110
34	133.8	17.9	495	14	AAQ04077
35	120.4	16.1	610	21	AAAB16224
36	118.2	15.8	441	11	AAQ05622
37	107.2	14.4	519	14	AAQ04078
38	96.4	12.9	716	21	AAZ98838
39	94	12.6	94	19	AAV46419
40	94	12.6	94	19	AAV30281
41	92	12.3	622	21	AAAB16219
42	86.4	11.6	659	21	AAAB16314
43	83.6	11.2	277	21	AAQ10817
44	73.4	9.8	306	12	AAQ14622
45	63.4	8.5	568	21	AAZ99185

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	17	AA136612
2	586	78.4	586	21	AA299822
3	536	71.8	536	19	AAV46422
4	536	71.8	536	19	AAV30284
5	304.8	40.8	763	19	AAV58279
6	304.8	40.8	859	20	AAZ34271
7	304.8	40.8	859	21	AACT8569
8	286.6	39.7	797	15	AAO69201
9	296.6	39.7	940	21	AACT7777
10	291	39.0	756	19	AAV5234
11	287.2	38.4	798	12	AAQ14623

PI Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L:
 PI Vlnik AI:
 DR WPI: 1996-402318/40.
 DR P-PSDB; AAR98525.
 XX
 PT Mammalian islet neo:genesis associated protein - isolated by
 PT stimulating mammalian pancreas by wrapping in cellopheane, for
 PT treatment of diabetes, etc
 XX
 PS Claim 13; Page 26; 50pp; English.
 XX
 CC This is the nucleotide sequence encoding the hamster islet neogenesis
 CC associated protein (INGAP). The gene is isolated from pancreatic cells
 CC which are induced to proliferate upon wrapping pancreatic tissue in
 CC cellopheane. Wrapping of the pancreas stimulate proliferation of new
 CC endocrine cells which appear from duct epithelium. The INGAP gene was
 CC isolated from a cDNA library constructed from mRNA purified from
 CC cellopheane wrapped hamster pancreas using a differential display method
 CC to compare genes expressed in cellopheane-wrapped and control pancreas.
 CC The gene contains an open reading frame which encodes a protein of 175
 CC amino acids. The protein has structural homology to the pancreatitis
 CC associated protein (PAP)/HIF family of genes which is associated with
 CC pancreatic or liver adenocarcinoma, and to the Reg/PSP1/throstaline
 CC (PSP = pancreatic stone protein) family of gene which has been shown to
 CC stimulate pancreatic beta-cell growth and may be involved in pancreatic
 CC islet regeneration. The protein can be used to stimulate islet cell
 CC proliferation in (non-)insulin dependent diabetic mammals.
 XX
 SQ Sequence 747 BP; 198 A; 173 C; 158 G; 218 T; 0 other;

Query Match 100.0%; Score 747; DB 17; Length 747;
 Best Local Similarity 100.0%; Pred. No. 1.8e-223;

Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGACAGGTACATGATGCTTCCATGACCTCTGTAGAGATGCTTGATGCTGCT 60
 DB 1 ctgaaagacaggtacatgactgcttccatgacctctgtagagtgcttgatgctgct 60
 QY 61 TTCTGCTGATGCTTCTTCTTGGTGGAGAGAGATTCGAAAGAAAGCTGCTTC 120
 DB 61 tctctgctgactgcttcttcttgggtggaagtgaaatctcaagaacatgaccttc 120
 QY 121 TTACGATATACGCTGCTCAAGGCTCTAGCTATGCTGCTATGCTATGCTACTGAT 180
 DB 121 ttaacgataactgcttctcaaggctctgtagcctatggttccattgctatcactgat 180
 QY 181 TTGTATACACAGACAGCTGCTTAATGACAACTATCTGCCAGATGCAATTTCTCAGGACA 240
 DB 181 ttgtataccacagacagctgcttaatgacaaactatctgcagatgacttctcaaggaca 240
 QY 241 CTTGGCATTTCTTCTCTGCTGTAATTTACTCTGTCCTGTCCTGCTTGTGAAGAACAG 300
 DB 241 cctggcatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 300
 QY 301 TTGACGCGCTACACAGTACATCTGATGAGACTTCATGATCCCTCAGACATGATGATACCT 360
 DB 301 ttgacgcttaccacagtaactctgacttgatccatgactccctccatgactgactacc 360
 QY 361 CAACGGAAGTGATGAGAGAGAGCACTTCCATGCTGACCTTCTATTAAGTGGAGAG 420
 DB 361 caacggagtgatgagagagagcaacttccatgctgacaccttccatgacagagag 420
 QY 421 GAACCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 gaaccccttattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 480
 QY 481 TCAGAGTGAGAGATTTTATTTGTAATGAGCTTCCATATATGCAAAATTCAGGT 540
 DB 481 tcagagtgagagatTTTATTTGTAATGAGCTTCCATATATGCAAAATTCAGGT 540
 QY 541 CTGAGGACAGTTCTTAATTTCAACAGCTTGAAATATTATGAAAGCTCAATGACAGGAG 600

DB 541 ctgagagcttcaattcaattcaacagctgaaatataatgtaagctcactgagcaagag 600
 QY 601 CAAGTATGAGGATTTCACTCAGAGAGCAAGCTGCTGCTACACACCACTTCCCT 660
 DB 601 caagtatgaggatTTTCACTCAGAGAGCAAGCTGCTGCTACACCACTTCCCT 660
 QY 661 TATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 661 tatatcatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 720
 QY 721 AGAGAACAAAATTAATGTCATCAAC 747
 DB 721 agagaaacaaaataaatgctacacac 747

RESULT 2

AA299822 standard; cDNA; 586 BP.
 ID AA299822 standard; cDNA; 586 BP.
 XX
 AC AA299822;
 DT 12-JUL-2000 (first entry)
 DE
 XX cDNA sequence of human pancreatic beta cell growth factor (INGAP).
 KW Human: pancreatic beta cell growth factor; INGAP: regenerating gene;
 KW REG gene: chronic mucosal injury; Hs.111244 polynucleotide;
 KW ulcerative colitis; Crohn's disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200014283-A2.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99MO-US20098.
 XX
 PR 04-SEP-1998; 98US-0146969.
 XX
 PA (UNIT) UNIV WASHINGTON.
 XX
 PI Dieckgrafe BK;
 XX
 DR WPI: 2000-257019/22.
 XX

PT Diagnosing chronic mucosal injury such as ulcerative colitis and
 PT Crohn's disease comprises detecting expression levels of regenerating
 PT gene family and a gene represented by a Hs.111244 polynucleotide in a
 PT human body sample -
 XX
 PS Disclosure: Page 36; 42pp; English.

CC The present sequence represents the cDNA sequence of human pancreatic
 CC beta cell growth factor (INGAP). The INGAP gene is part of the
 CC regenerating (REG) gene family. In normal circumstances, REG genes are
 CC regionally expressed in low amounts in the small bowel and pancreatic
 CC epithelium. However, they are strongly expressed in regions of the colon
 CC involved with chronic mucosal injury. The specification describes a
 CC method for diagnosing chronic mucosal injury by detecting expression
 CC levels of the REG gene family and a gene represented by a Hs.111244
 CC polynucleotide in a human body sample. The methods are useful for
 CC diagnosing chronic mucosal injury such as ulcerative colitis and Crohn's
 CC disease by detecting expression levels of the REG gene family and
 CC a gene represented by a Hs.111244 polynucleotide, respectively, in a
 CC human body sample.
 XX

SQ Sequence 586 BP; 148 A; 132 C; 130 G; 176 T; 0 other;

Query Match 78.4%; Score 586; DB 21; Length 586;
 Best Local Similarity 100.0%; Pred. No. 3.2e-173;
 Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	71.8%	Score 536	DB 19	Length 558
Best Local Similarity	99.1%	Pred. No. 1.3e-157		
Matches 539	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	86	GTGAGGTGAAGAAATTCAAAAGAAAGTGCCTTTCCATACGTATAACCTGCCTCAAGC	145	
Db	3	gcgagtcocgaagaatctccaaaagaactgcctcttcacgataaacctgctccaaagc	62	
QY	146	TCTGTAGCCCTATGGTCTCTATTTGCTAATTCAGATTTTGATACCAAGACCTGGTCTAAT	205	
Db	63	tctgtagccctatggctctatctatgcattccactgcgattttgatccaaagaccgctcta	122	
QY	206	GCAGAAATATCCCTGCAGATGCATTTTCAGAGACACCTGGCATTTCTTCAGTACTGGT	265	
Db	123	gcagaaatattccctgcagatgcattctccagaacacggaattctctccagtaactg	182	
QY	266	GAATTAACCTTCGTGCTCCCTCCCTTGTAAGAAACAGTTTGACCGCCTTACAGTAACTGG	325	
Db	183	gaattactcttcgttctcctcttgtagaacagtttgagcgctaccagtaactc	242	
QY	326	ATTGCACTTCATGATCCCTCACATGTGTACACTACCCAAAGCAAGTGGATGGAATGGAC	385	
Db	243	attgcaacttcatactccctacatgltacataccaaagagtgatgtagaagtcgagc	302	
QY	386	AGTTCCATGTGCTGACTCTTCATTAACGGGAGAGAAACCTCTAATGCTGCTACCGT	445	
Db	303	agttccaatgctggaactctctataaactgggaggaacccctcatctgctgcagcgt	362	
QY	446	GGTATTGTGCAAGTTTCTCTCAGAAATCAGGTTTTCAGAAAGTGAAGATTTAATGT	505	
Db	363	ggtattgtgcaagtttctctcagaaatcaggtttccgaagtggaagatcttaattgt	422	
QY	506	GAAATGAGCTTCCCTATATCTGCAAAATTCAAAGGCTTAGGGCAGTTCTAATTTCAACAC	565	

Db	423	gaaatgagcttcctccatatactgcacaaattcaaggtcttaggcagcttctaattcaacagc	482
Qy	566	TTGAAATATTATGAGCTCATCATGAGCAAGAGCAAGTATGAGATTCTCAGCAGAG	625
Db	483	ttgaaatatattatgaagctacatcgagacaagaagaatgatgagattcaccctgaag	542
Qy	626	AGCA	629
Db	543	agca	546
RESULT 5			
AAV58279	ID	AAV58279 standard; cDNA; 763 BP.	
AAV58279;	AC		
AAV58279;	DT		
04-DEC-1998	DT	(first entry)	
Human pancreatitis-associated protein.	DE		
Human pancreatitis-associated protein; PAP-2; agonist; pancreatitis;	XX		
hyperlipasla; hyperinsulinism; antagonist; tumour; oesophagus;	KW		
intestine; metastases; Crohn's disease; ulcerative colitis;	KW		
antibody; probe; PCR primer; amplification; hybridisation;	KM		
inhibitor; ss.	KX		
Homo sapiens.	OS		
Key	FT	Location/Qualifiers	
CDS	FT	115..642	
	FT	/*tag= a	
	FT	/product= "human PAP-2"	
W09841633-A1.	XX		
24-SEP-1998.	XX		
20-MAR-1998;	XX	98WO-US05699.	
20-MAR-1997;	XX	97US-0822261.	
(INCY-) INCYTE PHARM INC.	XX		
Goli SK, Hillman JL;	XX		
WPI: 1998-521222/44.	DR		
P-PSDB; AAW71682.	XX		
New pancreaticitis-associated protein and related nucleic acid, vectors, transformed cells - antibodies, agonists and antagonists, for diagnosis, treatment and prevention of pancreatitis or other pancreatic diseases, cancers, ulcerative colitis and Crohn's disease			
Claim 5; Fig 1A-1B; 66pp; English.			
This is the nucleotide sequence of the human pancreatitis-associated protein (PAP-2), used in the method of the invention. The human PAP-2, and its agonists are used to treat pancreatitis (particularly to prevent or control associated bacterial infections) and other pancreatic diseases such as hyperlipasla and hyperinsulinism. Also PAP-2 and its agonists/antagonists can be used to treat or prevent tumours, e.g. of the pancreas, oesophagus or intestines, and/or metastases, also Crohn's disease and ulcerative colitis. PAP-2 is also used to raise antibodies and to screen libraries for specific-binding agents. Antibodies are used for diagnosis or monitoring of PAP-2-related diseases (in usual immunoassays), in competitive drug screens and to isolate PAP-2 from natural sources. PAP-2 derived probes or primers are used in standard amplification or hybridisation tests to diagnose PAP-2-related diseases; to identify related sequences; for genomic mapping and for screening for specific inhibitors.			

SQ Sequence 763 BP; 182 A; 202 C; 197 G; 181 T; 1 other;

Query Match	40.8%;	Score 304.8;	DB 19;	Length 763;
Best Local Similarity	67.1%;	Pred. No. 2.8e-85;		
Matches 432;	Conservative	0;	Mismatches 212;	Indels 0;
			Gaps	0;

QY	9	CAGGTACCAAGATGCTTCCCATCCATCCCTGTGAGGATGTCCTTGAGATGCTGCTTCCGCC	66
Db	107	cagaacatcgtccctcccatcgtccctcgcacgtgtgtctcgtatgctgtcgtcttcctgc	166
QY	69	TGATGTTCCCTTCTTGGGTGGAAAGGTGAGAGATCTCAAAAGAAATGCTCTTCTCACGTA	128
Db	167	tcatctccctgtgtcaggttccaaagtgaagaacccagaaggaatcgtccctccccaaga	226
QY	129	TAAACCTGCTCMAAGGCTCTGTAGCCCTAGTGGGTCATTTGCTATTCACGATTTTGATAC	188
Db	227	tcagctgtcccaagaaggtcccaagacctatgtctccctcgtcatgtcttlttltcac	286
QY	189	CACAGACCTGGTGTAAATGACGAACATATCTCCACAGATGCAATTTCTACAGACACCTGGCAT	248
Db	287	caaatccctgtatgtgatgcagatctgtcgtccagaagcgccctctcgsaaactgtgt	346
QY	249	TTCCTTCCAGTACTGGTGAATAATTAACCTGCTGTCTCTCCCTTGTGAAGAACATTTACGGS	308
Db	347	ctgtgtccagttggtgtgaggtgaatcccttctgtctccctgtgtgagtagattagtaaca	406
QY	309	CTTACCGTATCACTGGATTGGATGGATCCATGATCCCTCACATGGTATACACTCCCAAGGAA	368
Db	407	gtactcatcatcctgtatctgtgtccatcabaaccccaacagggctcttgaccctgaatgag	466
QY	369	GTGGATGGAAGTGGAGACGATTCCAAATGCTGCACTTTATTAATGTGGAGAGAACCCCT	428
Db	467	atgtagtggagtgtagagcactgtatgtgtgaattacttctgatgtgaggaanaatccct	526
QY	429	CTATTGCTGCTGACCGCTGATTATTGTGCAATTTGTCTCGAAGAAATCAGGTTTTCAGAACT	488
Db	527	ccaccatcttaaacccctggccactgtgtgagcctgttcaagaagaacagatcttctgaagt	586
QY	489	GGAGACATTTTAATGTGGAATAATGAGCTTCCCTATATCTCAATTCACAAATTCAGGTAGGCA	548
Db	587	ggaaagattataactgtgtatgcaaaagttaacctatgtctgtcaagttcaaggaactaaggca	646
QY	549	GTTCTTAATTTCAACAGCTTGAAAAATATTATGAAGCTTCACATGGACAAGCAAGCAAGTATG	608
Db	647	gtgtggagatgcagagcctcagcttgtgcgtgcagctcatcatgacatgtgaccaggtgt	706
QY	609	AGGATTTACTTCAGGAAGACGAACGCTGTGCTTACATACACCCACACAC	652
Db	707	aagaactaaccttgaagaagataatctccccaactgtccctcac	750

RESULT	6
AAZ34271	
ID	AAZ34271 standard; cDNA; 859 BP.

AC AAZ34271;

DT 07-DEC-1999 (first entry)

DE Human PRO162 nucleotide sequence.

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

KW secreted protein; transmembrane protein; ss.

05 Homo sapiens.

PN WO9946281-A2.

PD 16-SEP-1999.

PF 08-MAR-1999; 99WO-US05028

XX	10-MAR-1998;	9805-0077450;
PR	11-MAR-1998;	9805-0077632;
PR	11-MAR-1998;	9805-0077641;
PR	11-MAR-1998;	9805-0077649;
PR	12-MAR-1998;	9805-0077791;
PR	13-MAR-1998;	9805-0078004;
PR	17-MAR-1998;	9805-0040720;
PR	20-MAR-1998;	9805-0078886;
PR	20-MAR-1998;	9805-0078810;
PR	20-MAR-1998;	9805-0078336;
PR	20-MAR-1998;	9805-0078939;
PR	25-MAR-1998;	9805-0079294;
PR	26-MAR-1998;	9805-0079656;
PR	27-MAR-1998;	9805-0079663;
PR	27-MAR-1998;	9805-0079664;
PR	27-MAR-1998;	9805-0079689;
PR	27-MAR-1998;	9805-0079686;
PR	27-MAR-1998;	9805-0079728;
PR	27-MAR-1998;	9805-0079768;
PR	30-MAR-1998;	9805-0079920;
PR	30-MAR-1998;	9805-0079923;
PR	31-MAR-1998;	9805-0080105;
PR	31-MAR-1998;	9805-0080107;
PR	31-MAR-1998;	9805-0080165;
PR	31-MAR-1998;	9805-0080194;
PR	01-APR-1998;	9805-0080327;
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PR	01-APR-1998;	9805-0080333;
PR	01-APR-1998;	9805-0080334;
PR	08-APR-1998;	9805-0081049;
PR	08-APR-1998;	9805-0081071;
PR	09-APR-1998;	9805-0081193;
PR	09-APR-1998;	9805-0081205;
PR	09-APR-1998;	9805-0081229;
PR	15-APR-1998;	9805-0081817;
PR	15-APR-1998;	9805-0081858;
PR	15-APR-1998;	9805-0081932;
PR	15-APR-1998;	9805-0081955;
PR	21-APR-1998;	9805-0082569;
PR	21-APR-1998;	9805-0082658;
PR	22-APR-1998;	9805-0082700;
PR	22-APR-1998;	9805-0082704;
PR	22-APR-1998;	9805-0082604;
PR	22-APR-1998;	9805-0082604;
PR	23-APR-1998;	9805-0082767;
PR	23-APR-1998;	9805-0082796;
PR	27-APR-1998;	9805-0083332;
PR	28-APR-1998;	9805-0083326;
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PR	30-APR-1998;	9805-0083559;
PR	05-MAY-1998;	9805-0083742;
PR	05-MAY-1998;	9805-0084366;
PR	06-MAY-1998;	9805-0084414;
PR	06-MAY-1998;	9805-0084441;
PR	07-MAY-1998;	9805-0084598;
PR	07-MAY-1998;	9805-0084600;
PR	07-MAY-1998;	9805-0084603;
PR	07-MAY-1998;	9805-0084637;
PR	07-MAY-1998;	9805-0084637;
PR	07-MAY-1998;	9805-0084640;
PR	07-MAY-1998;	9805-0084643;
PR	13-MAY-1998;	9805-0085123;
PR	13-MAY-1998;	9805-0085123;
PR	13-MAY-1998;	9805-0085338;
PR	13-MAY-1998;	9805-0085338;
PR	15-MAY-1998;	9805-0085573;
PR	15-MAY-1998;	9805-0085573;

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PR 15-MAY-1998; 9805-0085580.
PR 15-MAY-1998; 9805-0085582.
PR 15-MAY-1998; 9805-0085689.
PR 15-MAY-1998; 9805-0085697.
PR 15-MAY-1998; 9805-0085700.
PR 15-MAY-1998; 9805-0085704.
PR 18-MAY-1998; 9805-0086023.
PR 22-MAY-1998; 9805-0086392.
PR 22-MAY-1998; 9805-0086414.
PR 22-MAY-1998; 9805-0086430.
PR 22-MAY-1998; 9805-0086486.
PR 28-MAY-1998; 9805-0087098.
PR 28-MAY-1998; 9805-0087106.
PR 28-MAY-1998; 9805-0087208.
PR 30-JUL-1998; 9805-0094651.
PR 11-SEP-1998; 9805-0100038.
XX
XX (GETH ) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI: 1999-551358/46.
XX
XX P-PSDB; AAY41755.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 2; Fig 182; 530pp; English.
XX
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AAZ3891 to
XX AAZ3438, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX Sequence 859 BP; 223 A; 220 C; 193 G; 223 T; 0 other:
SQ

```

```

Query Match          40.8%; Score 304.8; DB 20; Length 859;
Best Local Similarity 67.18; Pred. No. 2.9e-85;
Matches 432; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

```

```

QY 9 CAGGTACCATGATGCTTCCCATGACCTCTGTAGATGCTTGGATCGCTCTTCTGCC 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 78 caggaactatgctgctcccatgctcctgctcctgctcctgctcctgctcctgctc 137
QY 69 TGATGTTCTTTCTTGGTGGAGAGTGAAGATCTCAAGAACTGCTTCTTCACTA 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 tcatctccctgctgctcctgctcctgctcctgctcctgctcctgctcctgctc 197
QY 129 TAACCTGCTCAGAGCTCTGTACCTATGAGGCTCTTGTGATTAATCTTGTATAC 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 198 tcaagctgctcctgctcctgctcctgctcctgctcctgctcctgctcctgctc 257
QY 189 CACAGACCTGGTCAATGCAAGATATCTGCGAGATGCTTCTGAGACACTGACAT 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 caaatcctctgagatgctgctgctgctgctgctgctgctgctgctgctgctg 317
QY 249 TTCTTCTAGTACTGTGAAATTAATCACTTCTGCTCTCTTGTGAGAACAGTTTGA 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 ctgctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 377
QY 309 CTAACGACGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 gctactacatcatctgctgctgctgctgctgctgctgctgctgctgctgctg 437

```

```

QY 369 GTGATGGAAGTGAGCAGCTTCCATGCTGACCTTCTATTACTGGAGAGAACCCCT 428
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 atgagtgaggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 497
QY 429 CTATTGCTGCTGACCGTGCGTTTATGTCAGATTTGTCTCAAGAAATCAAGTTTCA 488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 498 ccaccatcttaaacctctgctgctgctgctgctgctgctgctgctgctgctgct 557
QY 489 GGAGAGATTTTAAATTTGAAATGAGCTTCCCTATCTCAATTAATTAAGTCTAGGCA 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 558 ggaagagatlaatactgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 617
QY 549 GTTCTAATTTCAACAGCTTGAATAATTAATTAATTAATTAATTAATTAATTAAT 608
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 618 gctggaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 677
QY 609 AGGATTCACCTCAGGAGAGCAGCTCTGCTTACACACCCACAC 652
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 678 aagactacacctggaagagaatattctcccaactgacctacc 721

```

RESULT 7

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AAC78569
ID AAC78569 standard; cDNA; 859 BP.
XX
XX AAC78569;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Human PRO162 (UNQ429) nucleotide sequence SEQ ID NO:451.
DE
XX
XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
KW expressed sequence tag; detection; cancer; ss.
OS Homo sapiens.
XX
XX WO200053756-A2.
PN
XX
XX 14-SEP-2000.
PD
XX
XX 18-FEB-2000; 2000MO-US04341.
PF
XX
XX 08-MAR-1999; 99MO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99MO-US28313.
PR 02-DEC-1999; 99MO-US28551.
PR 02-DEC-1999; 99MO-US28565.
PR 16-DEC-1999; 99MO-US30095.
PR 30-DEC-1999; 99MO-US31243.
PR 30-DEC-1999; 99MO-US31274.
PR 05-JAN-2000; 2000MO-US00219.
PR 06-JAN-2000; 2000MO-US00277.
PR 06-JAN-2000; 2000MO-US00376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deansoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI: 2000-611443/58.
XX
XX P-PSDB; AAB44311.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,

```

PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -

PS Claim 2; Fig 1B2; 636pp; English.

XX AAC7458 to AAC7859 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC peptides. The PRO polynucleotides and polypeptides have cytosolic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC7860 to AAC7897 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.

XX Sequence 859 BP; 223 A; 220 C; 193 G; 223 T; 0 other;

Query Match 40.8%; Score 304.8; DB 21; Length 859;

Best Local Similarity 67.1%; Pred. No. 2.9e-85;

Matches 432; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 9 CAGGTACCATGATGCTCCATGACCTCTGTAGATGCTTGGATGCTGCTTCTGCC 68
DB 11
78 cagacataatgctccctccatgctccctgctccctgctccctgctccctgctccctgctcc
QY 69 TGATGTTCTTCTTGGGTGGAAGTGAAGATCTCAAGAAAGTCCCTTCTTCACTA 128
DB 11
138 tcaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 129 TAACTGCTCCAGGCTCTGTAGCTATGAGGCTCTGTAGATGCTTGGATGCTGCTTCTGCC 188
DB 11
198 tcaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 189 CACAGACCTGGTCTTAATGCAAGATCTGCGAGATGATCTTCTTCAAGACCTGGCAT 248
DB 11
258 caaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 249 TTCTTCTCACTGCTGGAATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 308
DB 11
318 ctgctccatgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 309 CCTTCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
DB 11
378 gctccatgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 369 GTGATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 428
DB 11
438 atgataatgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 429 CTATGCTGCTGACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
DB 11
498 ccaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 489 GGAGAGATTTAATTTGAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
DB 11
558 ggaagatataatgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 549 GTTCTAATTTCAACAGCTTGAATAATGATGATGATGATGATGATGATGATGATGATGATGAT 608
DB 11
618 gctgataatgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 609 AGGATTTCACTGAG 652
DB 11
678 aagatcactcctggaag

RESULT 8

AA069201 ID AA069201 standard; DNA: 797 BP.

XX

AC AA069201;

XX 21-FEB-1995 (first entry)

XX Human Pancreatitis-Associated Protein coding sequence.

XX Human PAP; pancreatitis-associated protein; diagnosis; detection;

XX cystic fibrosis transmembrane conductance regulator; CFTR gene;

XX mucoviscidosis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 43..570

XX polyA_signal

XX MO9415218-A.

XX 07-JUL-1994.

XX 23-DEC-1993; 93WO-FR01299.

XX 24-DEC-1992; 92FR-0015730.

XX (INRM) INST NAT SANTE & RECH MEDICALE.

XX Dagorn J, Iovanna J, Kelm V, Saries J;

XX WPI; 1994-234870/28.

XX P-PSDB; AAR57117.

XX In vitro detection of pancreatic disease associated with CFTR

XX gene mutation - by measuring concn. of pancreaticitis associated

XX protein in blood etc., suitable for neonatal diagnosis of, e.g.

XX cystic fibrosis

PS Claim 1; Fig 3; 33pp; French.

XX Antibodies which recognise the previously isolated and sequenced

XX human Pancreatitis-Associated protein (PAP) are claimed. They are

XX useful for measuring the amount of PAP in a sample to detect

XX pancreatic disease associated with heterozygotic mutations in the

XX CFTR gene. Such conditions result in expression of PAP at levels

XX at least 2-3 times higher than normal.

XX Sequence 797 BP; 180 A; 213 C; 198 G; 206 T; 0 other;

Query Match 39.7%; Score 296.6; DB 15; Length 797;

Best Local Similarity 65.8%; Pred. No. 1e-82;

Matches 431; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 9 CAGGTACCATGATGCTCCATGACCTCTGTAGATGCTTGGATGCTGCTTCTGCC 68
DB 11
35 cagacataatgctccctccatgctccctgctccctgctccctgctccctgctccctgctcc
QY 69 TGATGTTCTTCTTGGGTGGAAGTGAAGATCTCAAGAAAGTCCCTTCTTCACTA 128
DB 11
95 tcaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 129 TAACTGCTCCAGGCTCTGTAGCTATGAGGCTCTGTAGATGCTTGGATGCTGCTTCTGCC 188
DB 11
155 tcaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 189 CACAGACCTGGTCTTAATGCAAGATCTGCGAGATGATCTTCTTCAAGACCTGGCAT 248
DB 11
215 caaatccctgctgctccatgctccatgctccatgctccatgctccatgctccatgctcc
QY 249 TTCTTCTCACTGCTGGAATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 308
DB 11

Db 275 ctgtgctcaatgagggctgagatcccttcgtctccctccctgagagacatgtaaca 334
QY 309 CCAACCGTACATCTGATTTGATGATCCATGATCCCTACATGATGACACTACCAACGGAA 368
Db 335 gctactcaatcagcttgatggtgctcattgacccacagggacagcccaatgag 394
QY 369 GTGATGGAATGGAGACGATTTCCAAATGCTGACCTTCTAATCTAATCTGAGGAGAACCCCT 428
Db 395 aaggttgagggatgagtagcagatgtagtgaatcttctgcatgaggaagaatccct 454
QY 429 CTATTGCTGCTGACCGTGCTTATTGTCACGTTTGTCTCAAAATCAGTTTCAGAGT 488
Db 455 ccacacatcaagcccccgcacagtgcgagccatgagagaacagcagcttctgaggt 514
QY 489 GGAGAGATTTTAATGCAAAATGAGCTTCCATATCTATCTCAATTAATCAAGCTTAGGGCA 548
Db 515 ggaagagattacactgaaagtgaaggttaccctatgctcgaagttcactgactagtgca 574
QY 549 GTTCTAATTTTCAACAGCTTGAATAATATTATGAGCTCAGTCACATGGAACAAGCAAGTATG 608
Db 575 ggaagggaagtcagcagacgtgtgtgtgtgcaactcatcatatgagcagtgagaccagtggtg 634
QY 609 AGGATTCACCTACAGGAGAGCAAGCTCTGCTACACACCCACCAATTCCTTAT 663
Db 635 aggactcaccctggaagagatatatcgcttaattcccccaacctgaccacccat 689

RESULT 9
AAC77777
ID AAC77777 standard; cDNA; 940 BP.
XX AAC77777;
XX
XX AAC77777;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human cancer associated gene sequence SEQ ID NO:171.
XX
XX Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;
XX antidiabetic; antiaslathmic; antirheumatic; antiarthritic; antiviral;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; coagulant;
XX dermatologic; neuroprotective; thrombolytic; coagulant; noctropic;
XX vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
XX immune disorder; haematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200055350-A1.
XX
XX PD 21-SEP-2000.
XX
XX PF 08-MAR-2000; 2000MO-US05882.
XX
XX PR 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Ruben SM;
XX
XX DR WPI: 2000-587533/55.
XX
XX P-PSDB; AAB43568.
XX
XX PT Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
XX Claim 1: Page 750; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
XX CC in AAB4398 to AAB44239. The proteins can have activities based on the
XX CC tissues and cells the genes are expressed in. Example of activities

CC include: cytostatic; proliferative; vulnerability; immunomodulator;
CC antidiabetic; antiaslathmic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatologic; neuroprotective; coagulant; thrombolytic; coagulant;
CC noctropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies, and
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 940 BP; 287 A; 223 C; 203 G; 222 T; 5 other;
SQ

Query Match 39.7%; Score 296.6; DB 21; Length 940;
Best Local Similarity 65.8%; Pred. No. 1,1e-82;
Matches 431; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 9 CAGTACCATGATGCTTCCATGACCCCTCTGTAGATGTCCTTGATGCTGCTTCTGCGC 68
Db 70 cagacacatctgctcctccatccatgacctgcccagtgatcttgagatgctgctctgccc 129
QY 69 TGAATGCTCTTCTGAGGAGTGAAGAAATCTCAAAAGAACTGCTTCTACAGTA 128
Db 130 tcatgtctgtctcaggttcaagtgaaagaaacccagggagacgctcctgcacgga 189
QY 129 TAACGTGCTCCTCAGGCTGTGATGACCTATGAGTCTATTGCTATTTCAGTATTTGATAC 188
Db 190 tccgctcccaagagctccaagcctatgctccacatgctatgctctgttttctcacc 249
QY 189 CACAGACGTCGTATATGAGAACTATCCTGCCAGATGATTTCTCAGAACCTGGCAT 248
Db 250 caaatacccggaagatgagatcctgctcgaagaagggcccttggaacacctggt 309
QY 249 TTCTTCTCAGTCTGCTGAAATTAATTCCTTGCTGCTCCTTGTGAGAACAGTTGACGG 308
Db 310 ctgtgtcagtgagggtgagatcccttctgctccctcctgtgaaagacattgtgaaca 369
QY 309 CCTACCATGATCTGGATTGAGCTCCATGATCCTCAGATGCTACATGCTACCTAACCGGA 368
Db 370 gctactcatacgtcttgatggtctccacgacacacagggcaccgagcccaatgag 429
QY 369 GTGATGGAATGGAGACGATTCCAATGCTGCTGACCTTCTAATCTGAGGAGAACCCCT 428
Db 430 aaggttgagggatgagtagcagtgatgtagtaattacttcatatgaggaagaacccct 489
QY 429 CTATTGCTGCTGACCGTGCTTATTGTCAGATTTTGTCTCAAAATCAGTTTCAGAGT 488
Db 490 ccacacatcccaagcccccgcacagtgtgcagacctgcgagaagacacagatcttgaggt 549
QY 489 GGAGAGATTTTAATGCAAAATGAGCTTCCATATCTGCAAAATCAAGCTTAGGGCA 548
Db 550 ggaagagattacactgaaagtgaaggttaccctatgctcgaagttcactgactagtgca 609
QY 549 GTTCTAATTTTCAACAGCTTGAATAATATTATGAGCTCAGTCACATGGAACAAGCAAGTATG 608
Db 610 ggaagggaagtcagcagacgtgtgtgtgtgcaactcatcatatgagcagtgag 669
QY 609 AGGATTCACCTACAGGAGAGCAAGCTCTGCTACACACCCACCAATTCCTTAT 663
Db 670 aggactcaccctggaagagatatatcgcttaattcccccaacctgaccacccat 724

RESULT 10
AAV35234

ID AAV35234 standard; cDNA to mRNA; 756 BP.
 XX
 AC AAV35234;
 XX
 DT 15-SEP-1998 (first entry)
 XX
 DE Mouse FLS-ob/ob cDNA.
 XX
 KW Fatty liver Shionogi; FLS; obese gene; ob gene; model; disease; obesity;
 liver; disorder; hyperlipidemia; type II diabetes; hepatoma;
 triglyceride-associated cirrhosis; ds.
 KW
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 32..559
 FT /*tag= a
 FT /product= -ob/ob protein
 FT
 XX MO9819523-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 30-OCT-1997; 97WO-JP03948.
 XX
 PR 01-NOV-1996; 96JP-0291555.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Makino S, Oshima I, Soga M;
 XX
 DR WPI: 1998-286457/25.
 XX
 PT Model mouse for type II diabetes and liver diseases - derived from
 PT inbred FLS mouse strain by insertion of variant ob gene from type II
 PT diabetic mouse
 PT
 XX
 PS Claim 2; Fig 6; 37pp; Japanese.
 PS
 XX
 CC This cDNA sequence is a novel variant mouse obesity (ob) gene. this
 CC sequence is used in a method resulting in a model mouse for human
 CC diseases associated with lipid disorders e.g. obesity, liver cirrhosis,
 CC hyperlipidemia, type II diabetes and hepatoma. The variant ob gene is
 CC inserted into a mouse lacking this gene, such as an inbred FLS (Fatty
 CC Liver Shionogi) mouse. The variant is derived from a type II diabetic
 CC mouse strain such as C57BL/6J-ob/ob, and the gene is inserted into the
 CC FLS strain by cross-breeding the two strains then breeding back to FLS
 CC for several generations with selection for ob-bearing individuals in each
 CC generation. The model mouse obtained may be homozygous or heterozygous
 CC for the ob gene. The heterozygous mouse when reared under normal
 CC conditions develops triglyceride-associated cirrhosis of the liver from
 CC infancy, and when older develops hepatoma. The homozygous mouse
 CC (FLS-ob/ob) shows severe diabetes in both males and females at 5-15
 CC weeks, a considerable increase in body weight in both males and females
 CC from infancy onwards, very high blood sugar levels from infancy to 20
 CC weeks, high blood insulin levels, sugar resistance abnormalities, blood
 CC hyperlipidemia (cholesterol, triglycerides and phospholipids) from
 CC infancy to 20 weeks, liver cirrhosis (triglyceride-associated) from
 CC infancy onwards and the development of hepatoma when old.
 CC
 XX
 SQ Sequence 756 BP; 201 A; 184 C; 167 G; 204 T; 0 other;

Query Match 39.08; Score 291; DB 19; Length 756;
 Best Local Similarity 66.68; Pred. NO: 5.6e-81;
 Matches 431; Conservative 0; Mismatches 215; Indels 1; Gaps 1;

OY 1 CTGCAAGACAGTACCATGATCTCCATGACCTCTGTAGAGTCTTGGATGCTGCT 60
 ||| ||||| | ||||| ||| | ||| ||||| ||||| ||||| ||||| |||||
 Db 16 ctggaagacagacagatgctgctcccaacagcgtcgtccgtcgtcgtgagtctgct 75
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 61 TTCTGCTGATGTTCTTTCTTGGGTGAAGGTGAAGAAATCTCAAAAGAACTGCCCTTC 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 76 ctctgctgctgctgtcttattctcaagltcaagtgtagaagctccctggaatataccctc 135
 OY 121 TTCAAGTATTAACCTGTCCCTCAAGGCTCTGTAGCCCTATGCTTATTCACCTGAT 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 136 cgcagacatgtagtggccccaaggtctcccaagcttatgctccctactctttagctt 195
 OY 181 TTGTATCCACAGACACTGGTCTTAATGACAACTATCTCTGCCAGATGATTTCTCAGACA 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 196 tcaaglacacagacctgtgttagtcagaacctggtccgcgaagaagagcctgtagagaca 255
 OY 241 CCTGGCATTTTCTTCACACTACTGCTGGAATATACCTGCTGTCTCCCTTGGAAGAACAG 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 256 cctgctatcgtgctccaatagcgtgagctcattcctcctcccaatgtagaagagac 315
 OY 301 TTTGACGGCTCTACACAGTACATCTGGATTGACATCCATGATCCCTACATGCTACACTAC 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 316 acgaacacagctacacatacacttgatgttggtctccatgaccccaactcgtgtagaac 375
 OY 361 CAACGGAAGTGATGGAAGTGAGCAGTTCACAAATGCTGACCTTCTATTAACCTGGAGAG 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 376 caatgycgtgtagtggatgtagaagtagaacaatgacgtgtagaattacttaacttagagag 435
 OY 421 GAACCCCTCTAATGCTGCTGACCCGCTGTTATTTGCTGACATTTTGTCTCAGAAATCAGGTT 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 436 gaaccacactactgctcttagaccgtgcttctgtagaagctgtcaagaagcttcgagatc 495
 OY 481 TCAGAGTGGAGAGATTATTTAATTTGAAATGAGCTTCCCTATATCTCAAAATTCAGAGT 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 496 tctaaatgtagagatagacatgtagagtgtagagtgtagagtgtagagtgtagagtgtagag 555
 OY 541 CTAGGGAGTCTTAATTTCAACAGCTTGAATAATATATGAGCTCA-CATGACACAGGAA 599
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 556 ttaacttactcagacagacaacatccgaattgtcttgaagagcatcatgacagaagga 615
 OY 600 GCAACTATGAGATTCATCTACAGAGACAGCAAGCTGTGCTACACACC 646
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 616 caaatgtggaagactcactagaaaagcatlcttacttactcagatcc 662

RESULT 11

AAQ14623 standard; DNA; 798 BP.

AAQ14623;

29-JAN-1992 (first entry)

Fragment S4 from human pancreatitis associated protein gene.

hPAP; pancreas; imaging; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 43..567

/*tag= a

/product= human PAP

W09116428-A.

31-OCT-1991.

18-APR-1991; 91WO-FR00323.

20-APR-1990; 90FR-0005062.

(INRM) INSERM INST NAT SANTE.

Iovanna JL, Keim V, Dayron JC;

WPI: 1991-339816/46.

P-PSDB; AAR14795.


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PR 16-SEP-1998; 98GB-0020193.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Livesey FJ, Hunt SP;
PI
XX MPI; 2000-567204/53.
DR
XX P-PSDB; AAB18614.
XX
XX New Schwann cell mitogen (known as Reg-2), useful for repair and
PT regeneration of neuronal cells and tissue, is upregulated during
PT neuronal regeneration.
XX
XX Disclosure; Page 24; 32pp; English.
XX
XX The present sequence encodes a Schwann cell mitogen, known as Reg-2.
CC Reg-2 can be upregulated during regeneration of neuronal cells and
CC tissue. Reg-2 is an essential component in neuron-glia interaction
CC that underlies development and regeneration of mammalian motor
CC neurons. It is a 16 kDa protein. Reg-2 is used to affect development
CC of neuronal cells and tissue, especially for promoting their repair
CC and regeneration, particularly of motor cells in adult humans.
XX
XX
SQ Sequence 781 BP; 221 A; 181 C; 177 G; 202 T; 0 other;

Query Match      38.4%; Score 286.8; DB 21; Length 781;
Best Local Similarity 65.4%; Pred. No. 1.2e-79;
Matches 420; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

QY 5 AAGACAGGTACGATGATCTTCCATGACCCCTGTAGATGCTTGGATGCTGCTTCC 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 atgagagtaataatgtgatctgctgcttccagctatgctgctgctgcttcc 109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 TGCCTGATGCTCTTCTTGTGGTGGAAGTGGAAGATCTCAAAAAGAACCTCTTCA 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 tgcctgatgctcttctatcagagtgcaagagaccttcgaagaaataacacctcgca 169
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 CGATTAACCTGCTCTCAAGGCTCTGTAGCCATGGGCTCTATTGCTTTCAGATTTG 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 170 cgaatagtgccccaagagcccaagcatalagctcccaagctatgctgcttccag 229
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 ATACACAGACCTGCTCTATGATGAGAACTATCTCCAGATGATTTCTAGACACCTG 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 ataccagaagccgtgttgctgcaagactgctgccaagagagactcgtgaagacactc 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 GCATTTCTTCTCAGTACTGCTGAAATTAACCTGCTGCTCCCTTGGAAGAACGTTTG 304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 290 gtatctgtctcaatgagctgcaagcttcttgccatcccaagctgcaagaaacatgga 349
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 305 ACGGCTTACAGATCATCTGGATTTGACATGATCCCTACATGCTATACCTACCCAC 364
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 350 aacagctaacataatagctgagctgacccacagcacccttgctgagagaccacat 409
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 365 GGAAGTGATGAGAGTGAGACAGTCCATATGTGCTGACCTTATATACCTGGAGAGAAC 424
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 410 gggagtgagatggagtgagtgaaatgacataatgataatgtaacactgaggaggaac 469
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 425 CCTCTATTCTCTCTGACCTGCTGTTATTTGACAGTTTGTCTCAAGAAATCAGGTTTTCAG 484
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 470 ccaatctactctcttagacccgagatctctgagacgttgcaagatctcttgatctcta 529
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 485 AATGAGAGATTTTATTTGTAATGAGCTTCCCTATATCTGCAATTTCAAGAGCTTAG 544
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 530 agatgagagataccaatgtaagtgagtgccctacgctcgcaaatcttaagcttaa 589
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 545 GGCAGTTCTTATTTCAACACTGAAATATTTATGAAAGCTACATGGACAGAGAACG 604
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 590 aattaccagaagcaaacagctttagtttctcgtgaagcaccatccgtcaagggcaca 649
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 605 TATGAGATTTCACTCAGAGAGACCAAGCTCTGCTTACACAC 646
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 650 tatgaagacttgctgtaagaaagtatctatctacagctc 691
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 15
ID AA014621 standard; cDNA, 793 BP.
XX
XX AA014621;
AC
XX
XX 29-JAN-1992 (first entry)
XX
XX DE Fragment S1 encoding rat pancreatitis associated protein.
XX
XX hPAP; pancreas; imaging; ss.
XX
XX Rattus.
XX
XX Key Location/Qualifiers
FH sig_peptide 61..139
FT /tag- a
FT mat_peptide 140..613
FT /tag- b
FT /product- PAP
XX
XX WO9116428-A.
XX
XX 31-OCT-1991.
XX
XX 18-APR-1991; 91WO-PR00323.
XX
XX 20-APR-1990; 90PR-0005062.
XX
XX (INRM ) INSEPM INST NAT SANTE.
XX
XX Iovanna JL, Keim V, Dagron JC;
XX
XX MPI; 1991-339816/46.
XX
XX P-PSDB; AAR14797.
XX
XX cDNA fragment of human pancreatitis associated protein -
PT produced by genetic engineering, and the corresponding antibody,
PT for use in the diagnosis of pancreatitis
XX
XX Claim 8; Page 30; 49pp; French.
XX
XX The cDNA fragment S1 encodes the rat PAP. It
CC was isolated from a rat pancreatic cDNA library using antibodies
CC against rat PAP. The cDNA was used as a probe to screen a human
CC pancreatic cDNA library to identify human PAP sequences.
XX
XX
SQ Sequence 793 BP; 232 A; 181 C; 177 G; 203 T; 0 other;

Query Match      37.3%; Score 279; DB 12; Length 793;
Best Local Similarity 65.6%; Pred. No. 3.3e-77;
Matches 422; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

QY 5 AAGACGTAACATGATGCTTCCATGACCCCTGTAGATGCTTGGATGCTGCTTCC 64
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 atgagagtaataatgtgatctgctgcttccagctatgctgctgctgcttcc 109
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 65 TGCCTGATGCTCTTCTTGTGGTGGAAGTGGAAGATCTCAAAAAGAACCTCTTCA 124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 tgcctgatgctcttctatcagagtgcaagagactcctcgagaagaaatatacccttgca 169
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 CGTATAACCTGCTCTCAAGGCTCTGTAGCCATGGGCTCTATTGCTTATTCAGATTTTG 184
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 170 cgaatagtgccccaagagctccagacatagctcctactgctatgctgctgcttccag 229
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 ATACACAGACCTGCTCTATGATGAGAACTATCTCCAGATGATTTCTAGACACCTG 244
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 ataccagaagccgtgttgctgcaagactgctgccaagagagacttgagagacactc 289
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 245 GCATTTCTTCTCAGTACTGCTGAAATTAACCTGCTGCTCCCTTGGAAGAACGTTTG 304
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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